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(54) Title: 70 HUMAN SECRETED PROTEINS

(57) Abstract

The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.

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70 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoeitin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein , a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH_2PO_4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal poly(A) tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched , for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

The translation product of this gene shares sequence homology with DNA encoding allergens of Cladosporium herbarum, in addition to, the rat TSEP-1 protein (See Genbank Accession No. W12827) which is thought to be important in the modulation of MHC Class I gene expression. As such, protein product of this gene mae be beneficial in the prevention and treatment of auto-immune disease and transplant rejection. When tested against myelogenous leukemia cell lines, supernatants removed from cells containing this gene activated Calcium permeability. Thus, it is likely that this gene activates signal transduction pathways in myelogenous leukemia cells thro

intracellular calcium release. Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. Alterations in small molecule concentration can be measured to identify supernatants which bind to receptors of a particular cell. In specific embodiments, polypeptides of the invention comprise the sequence: FITPEDGSKDVFVHFSAISSQGFKTLAEGQRVEFEITNGAKGPSAANVIAI (SEQ ID NO:157). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in CD34-depleted white blood cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,allergy caused by Cladosporium herbarum, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.blood cells, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to DNA encoding allergens of Cladosporium herbarum indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of allergy caused by Cladosporium herbarum. Similarly, the tissue distribution in white blood cells, combined with the oberved calcium release activity in myelogenous leukemia cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in immune cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological

disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. The secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological acitivities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:11 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 378 of SEQ ID NO:11, b is an integer of 15 to 392, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

The translation product of this gene shares sequence homology with human histiocyte-secreted factor HSF, a tumor necrosis factor-related protein, which is thought to be important for its potential anti-tumor activity. When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon-

sensitive responsive element) pathway. Thus, it is likely that this gene activates leukemia cells through the Jaks-STAT signal transduction pathway. ISRE is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. The gene encoding the disclosed cDNA is believed to reside on chromosome 2. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 2.

This gene is expressed primarily in CD34 positive white blood cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for anti-tumor reagents. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.blood cells, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in CD34 positive cells, combined with its homology to the human HSF protein, in addition to the detected biological activity within leukemia cell lines, indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. The secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological acitivities. Typical of these are cytokine, cell proliferation/differentiation

modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:12 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 451 of SEQ ID NO:12, b is an integer of 15 to 465, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 3

This gene is expressed primarily in CD34 positive blood cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,diseases of the immune and hematopoietic systems, especially those of CD-34 positive bloodcells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.blood cells, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or

cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:86 as residues: Gly-7 to Asp-14, Ile-16 to Tyr-36, Lys-47 to Ser-54.

The tissue distribution in CD34 positive blood cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:13 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 660 of SEQ ID NO:13, b is an integer of 15 to 674, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene is expressed primarily in CD34 positive blood cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions:immune or hematopoietic disorders, particularly diseases of CD 34 positive cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hematopoietic systems, expression of this gene at significantly higher or lower levels

may be routinely detected in certain tissues or cell types (e.g.blood cells, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:87 as residues: Glu-12 to Thr-21.

The tissue distribution in CD34 positive white blood cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:14 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 283 of SEQ ID NO:14, b is an integer of 15 to 297, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 5

This gene is expressed primarily in Hodgkin's lymphoma tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,Hodgkin's lymphoma, or related immune or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in

providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.blood cells, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:88 as residues: Ser-36 to Cys-42.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in Hodgkin's lymphoma indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:15 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 590 of SEQ ID NO:15, b is an integer of 15 to 604, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 6

This gene is expressed primarily in placenta, embryo, and, to a lesser extent, in tonsil and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,diseases of the female reproductive system, or developing tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the female reproductive or immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.developing, reproductive, immune, and cancerous and wounded tissues) or bodily fluids (e.g.amniotic fluid, lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in placental and embryonic tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders, particularly of the female reproductive system. Similarly, expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Additionally, the expression in immune tissues indicates that this protein may play a role in the proliferation, differentiation, and/or survival of hematopoietic cell lineages. In such an event, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoictic lineages from early hematopoietic stem and committed progenitor cells. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Alternatively, expression within ovarian tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancreas (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-,hypoparathyroidism) ,

hypothallamus, and testes. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:16 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1132 of SEQ ID NO:16, b is an integer of 15 to 1146, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

This gene is expressed primarily in embryonic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,developmental disorders, in addition to cancer and other disorders characterized by proliferating tissues.Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of embryonic tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.developmental, proliferating, and cancerous and wounded tissues) or bodily fluids (e.g.amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:90 as residues: Ser-11 to His-16.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in

cancer therapy. The secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological acitivities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:17 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 664 of SEQ ID NO:17, b is an integer of 15 to 678, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

This gene is expressed primarily in kidney, and to a lesser extent, in other human tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,diseases of the kidney or urogenital system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the urinary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.urogenital, endocrine, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:18 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1291 of SEQ ID NO:18, b is an integer of 15 to 1305, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

This gene is expressed primarily in T-cell lymphoma and embryonic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,immune, developmental, or hematopoietic disorders, particularly T-cell lymphoma or other disorders characterized by proliferating tissues or cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected

in certain tissues or cell types (e.g.blood cells, immune, hematopoietic, developing, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cell lymphoma indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:19 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1046 of SEQ ID NO:19, b is an integer of 15 to 1060, where both a and b correspond to the

positions of nucleotide residues shown in SEQ ID NO:19, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in adipose tissue, and to a lesser extent, in other human tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,metabolic disorders, particularly those involving anomalous lipid metabolism. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of adipose tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.adipose, and cancerous and wounded tissues) or bodily fluids (e.g.bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:93 as residues: Tyr-25 to Thr-32.

The tissue distribution in adipose tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, prevention, and/or treatment of various metabolic disorders such as Tay-Sachs disease, phenylkenonuria, galactosemia, hyperlipidemias, porphyrias, and Hurler's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:20 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1156 of SEQ ID NO:20, b is an integer of 15 to 1170, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

This gene is expressed primarily in infant brain, and to a lesser extent, in human nine week old early stage.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neural degenerative or developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous or reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.developing, neural, and cancerous and wounded tissues) or bodily fluids (e.g.amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:94 as residues: Lys-50 to Asp-66, Pro-68 to Glu-77, Glu-102 to Glu-107, Glu-131 to Leu-146, Ala-175 to Glu-183, Phe-205 to Lys-216, Val-263 to Thr-281, Pro-304 to Ala-313.

The tissue distribution in infant brain indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:21 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2070 of SEQ ID NO:21, b is an integer of 15 to 2084, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

This gene is expressed primarily in atrophic endometrium.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,atrophic endometriosis, or other disorders of the female reproductive system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the female reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, uterine, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of atrophic endometriosis and related uterine disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:22 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 629 of SEQ ID NO:22, b is an integer of 15 to 643, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 13

This gene is expressed primarily in fetal tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,developmental abnormalities, or disorders characterized by proliferating tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.developing, proliferating, and cancerous and wounded tissues) or bodily fluids (e.g.amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:96 as residues: Gly-26 to Arg-37.

Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:23 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 633 of SEQ ID NO:23, b is an integer of 15 to 647, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

The gene encoding the disclosed cDNA is believed to reside on chromosome 19. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 19.

This gene is expressed primarily in epididymus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,male infertility. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.epididymus, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g.seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of male infertility, possibly related to low sperm motility. Similarly, expression of this gene product in the epididymous may implicate this gene product in playing a vital role in maintaining normal testicular function. As such, this gene product may find utility as a male contraceptive.Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:24 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 811 of SEQ ID NO:24, b is an integer of 15 to 825, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 15

This gene is expressed primarily in IL5-induced eosinophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,acute inflammation, or other immune disorders such as asthma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.blood cells, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in eosinophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, sepsis, acne, and psoriasis, asthma, and inflammatory disorders, such as inflammatory bowel disease. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:25 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 527 of SEQ ID NO:25, b is an integer of 15 to 541, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

This gene is expressed primarily in induced endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,arteriosclerosis, or other vasculature disorders, particularly microvascular disease and stroke. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.cardiovascular, and cancerous and wounded tissues) or bodily fluids (e.g. serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:99 as residues: Ser-33 to Arg-48, Gln-64 to Val-71, Pro-121 to Thr-132, Gln-167 to Lys-181.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of endothelial inflammation or occlusion due to arteriosclerosis. Similarly, the protein product of this gene may also show utility in the detection, treatment, or prevention of stroke, aneurysms, or other vascular disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:26 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of

a-b, where a is any integer between 1 to 838 of SEQ ID NO:26, b is an integer of 15 to 852, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 17

This gene is expressed primarily in ovarian cancer, and to a lesser extent, in infant brain, 12 Week old early stage embryo, and synovial hypoxia.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,developmental or proliferative disorders, particularly ovarian cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive or neural systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, developmental, skeletal, and cancerous and wounded tissues) or bodily fluids (e.g.amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:100 as residues: Ser-7 to Gly-17.

The tissue distribution within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Alternatively, expression within infant brain indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo. sexually-linked

disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:27 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4584 of SEQ ID NO:27, b is an integer of 15 to 4598, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

When tested against PC12 cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) pathway. Thus, it is likely that this gene activates sensory neuron cells through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jaks-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation.

This gene is expressed primarily in fetal brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,degenerative neural disorders or developmental disorders, particularly proliferative abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, developing, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:101 as residues: Val-16 to Asn-24.

The tissue distribution in infant brain combined with the detected biological EGR1 activity in sensory neurons indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:28 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 571 of SEQ ID NO:28, b is an integer of 15 to 585, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 19

The translation product of this gene was shown to have homology to the human zinc finger 91 which is thought to important in the regulation of gene expression (See Genbank Accession No. Q05481). The gene encoding the disclosed cDNA is believed to reside on chromosome 19. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 19.

This gene is expressed primarily in uterine cancer, and to a lesser extent in melanocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,reproductive disorders, particularly uterine cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a

number of disorders of the above tissues or cells, particularly of the reproductive or integumentary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, epithelial, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tumors of uterine origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Alternatively considering the expression within melanocytes indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e.wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, althletes foot, and ringworm). Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:29 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 810 of SEQ ID NO:29, b is an integer of 15 to 824, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

The translation product of this gene was shown to have homology to the human RAMP2 protein which is thought to be important in calcitonin regulation (See Genbank Accession No. gnl|PID|e1295011 (AJ001015)). In specific embodiments, polypeptides of the invention comprise the sequence: RAGGPRLPRTRVGRPAALRLLLLLGAVLNPHEALAQXLPTTGTPGSEGGTVKN XETAVQFCWNHYKDQMDPIEKDWCDWAMISRPYSTLRDCLEHFAELFDLGF PNPLAERIIFETHQIHFANCSLVQPTFSDPPEDVLLA (SEQ ID NO:158), CWN HYKDQMDPIEKDWCDWAMISRPYSTLRDCLEHFAELFDLGFPNPLAERIIFETH QIH (SEQ ID NO:159), FANCSLVQPTFSDPPEDVLLAMIIAPICLIPFLITLVV WRSKDSEAQA (SEQ ID NO:160), RAGGPRLPRT (SEQ ID NO:161), or NPHEA LAQ (SEQ ID NO:162). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in fetal kidney, spleen, and to a lesser extent in chronic synovitis and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,kidney, endocrine, urogenital, or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine or haemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.endocrine, urgenital, skeletal, cardiovascular, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:103 as residues: Arg-19 to Gln-26.

The tissue distribution in kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities, horseshoe kidney, polycystic kidney, and Falconi's

syndrome. Similarly, considering the homology to the RAMP2 protein, indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancrease (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper- ,hypoparathyroidism) , hypothallamus, and testes. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:30 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 759 of SEQ ID NO:30, b is an integer of 15 to 773, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neurodegenerative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, developing, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:104 as residues: Arg-29 to Ile-39.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative

disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:31 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 955 of SEQ ID NO:31, b is an integer of 15 to 969, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

The gene encoding the disclosed cDNA is believed to reside on chromosome 12. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 12.

This gene is expressed primarily in infant and adult brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neurodegenerative or developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, developing, proliferative, and cancerous and wounded tissues) or bodily fluids (e.g.amniotic fluid, lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level

expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:105 as residues: Arg-13 to Glu-22, Ser-34 to Phe-44, Ser-46 to Thr-52.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:32 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1341 of SEQ ID NO:32, b is an integer of 15 to 1355, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 23

This gene is expressed primarily in fetal dura mater.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neurodegenerative disorders, particularly spina bifita. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system,expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, developmental, proliferative, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum,

plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:106 as residues: Lys-15 to His-21.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, spina bifita, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:33 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 522 of SEQ ID NO:33, b is an integer of 15 to 536, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

The gene encoding the disclosed cDNA is believed to reside on chromosome 3. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 3.

This gene is expressed primarily in fetal liver, spleen, and to a lesser extent in ovary and glioblastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hepatic, immune, or haematopoietic disorders. Similarly, polypeptides

and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the haematopoietic or hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.hepatic, blood cells, immune, haematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). In addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various would-healing models and/or tissue trauma. Alternatively, expression within spleen tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:34 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer

between 1 to 1109 of SEQ ID NO:34, b is an integer of 15 to 1123, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

This gene is expressed primarily in brain frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neurodegenerative disorders, particularly those afflicting the frontal cortex. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:108 as residues: Ser-5 to Thr-11, Tyr-90 to Arg-96.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:35 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly,

preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 573 of SEQ ID NO:35, b is an integer of 15 to 587, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

This gene is expressed primarily in brain frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neurodegenerative disorders, particularly of the fronal cortex. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervouse system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:36 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly,

preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 828 of SEQ ID NO:36, b is an integer of 15 to 842, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 27

This gene is expressed primarily in brain frontal cortex, and to a lesser extent, in the epididymus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neurodegenerative disorders, particularly of the frontal cortex, or reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, urogenital, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the expression within the epididymus may suggest that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various reproductive disorders, particularly male infertility. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:37 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 939 of SEQ ID NO:37, b is an integer of 15 to 953, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 28

The translation product of this gene shares sequence homology with the human placental DIFF33-LIKE protein, in addition to the Diff33 gene product (See Genbank Accession Nos. gnl|PID|e1310269 dJ425C14.2 and gi|1293563, respectively). Both of these proteins are thought to be important in the regulation of cell-cycle control and growth within reproductive tissues and cells. In specific embodiments, polypeptides of the invention comprise the sequence: AQERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGN NSTVTRLIYALFLLVGVCVACVMLIPGMEEQLNKIPGFCENEKGVVPCNILVGY KAVYRLCFGLA (SEQ ID NO:163), IPCLCGSAPCLLCRCCPSGNNSTVTRLI YALFLLVGVCVACVMLIPGMEEQLNKIPGFCENEKGVVPCNILVGY (SEQ ID NO:164), ARSDGSLEDGDDVHRAVDNERDGVTYSYSFFHFMLFLASLYIMM TLTNWYRYEPSREMKSQWTAVWVKISS SWIGIVLYVWTLVAPLVLTNRDFD (SEQ ID NO:165), NEKGVVPCNILVGYKAVYRLCFGLAMFY (SEQ ID NO:166), MIKVKSSSDPRAAVHNGFW (SEQ ID NO:167), GMAGAFCFILIQLVLLIDFAH (SEQ ID NO:168), YAALLSATALNYLLSLVAIVLFFV (SEQ ID NO:169), PSLLSIIGYNTTSTVPKEGQS (SEQ ID NO:170), YSSIRTSNNSQVNKLTLTSDES (SEQ ID NO:171), DNERDGVTYSYSFFHFMLFL (SEQ ID NO:172), or IVLYVWTLVAPLVLTNRD (SEQ ID NO:173). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 20. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 20.

This gene is expressed primarily in thymus stomal cells, and to a lesser extent, in human T-cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to,reproductive disorders, particularly those involving proliferative cells, such as cancer and tumor growth. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and tumor growth in various tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, immune, cancerous and wounded tissues) or bodily fluids (e.g.lymph, seminal fluid, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:111 as residues: Lys-87 to Cys-95, Ala-126 to Asn-131, Ile-154 to Gly-162, Thr-182 to Asn-190, Ser-203 to Gln-210, Ser-234 to Asn-244, Gly-259 to Ser-266, Asp-278 to Val-284, Glu-313 to Gln-321.

The tissue distribution and homology to Diff33 gene product indicates that polynucleotides and polypeptides corresponding to this gene are useful for identifying or designing drug(S) targeted against cancers/tumors where unregulated growth is due, in part, to the overexpression of this gene product. Diff33 gene product is 2-15 fold overexpressed in testicular tumors from polyomavirus large T-antigen transgenic mice and thus may play a regulatory role in cell growth. Due to its strong homology to Diff33, this gene may have a similar regulatory role, not only in testicular or placental cancers, but within reprouctive tissues, in general. The secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological acitivities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for

regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:38 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2197 of SEQ ID NO:38, b is an integer of 15 to 2211, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:38, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed primarily in breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,reproductive disorders, particularly breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic and female reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.breast, reproductive, endocrine, and cancerous and wounded tissues) or bodily fluids (e.g.breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:112 as residues: Gly-13 to Pro-19, Pro-38 to Pro-46, Thr-49 to Gly-57.

The tissue distribution in tumors of breast origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Expression within cellular sources marked by proliferating cells indicates that this

protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:39 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 668 of SEQ ID NO:39, b is an integer of 15 to 682, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

The translation product of this gene shares sequence homology with the human ZN-alpha-2-glycoprotein, which is thought to important in the modulation of the immune response and possibly in the regulation of cell division (See Genbank Accession No. gil467671). In specific embodiments, polypeptides of the invention comprise the sequence: DPRVRADTMVR (SEQ ID NO:174), GPAVPQENQDGR YSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFR (SEQ ID NO:175), YNSKDRK SQPMGLWRQVEGME (SEQ ID NO:176), FMETLKDIVEYYNDSNGSHVLQ (SEQ ID NO:177), or NRSSGAFWKYYYDGKDYIEF (SEQ ID NO:178). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 7. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 7.

This gene is expressed primarily in liver, breast, and to a lesser extent, in spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,reproductive or immune disorders, particularly those involving cancer,

such as of the breast. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, hematopoietic, or reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, reproductive, hematopoietic, hepatic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:113 as residues: Val-16 to Tyr-25, Tyr-58 to Gln-66, Met-77 to Arg-90, Tyr-104 to Gly-110, Glu-123 to Ser-128, Tyr-135 to Asp-140, Ile-160 to Trp-165.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in spleen indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, expression within the liver indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). In addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various would-healing models and/or tissue trauma.Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of

these sequences are related to SEQ ID NO:40 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 671 of SEQ ID NO:40, b is an integer of 15 to 685, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 31

When tested against human Jurket T-cell lines, supernatants removed from cells containing this gene activated the NF-kB (Nuclear Factor kB) transcription pathway. Thus, it is likely that this gene activates T-cells through the NF-kB pathway. NF-kB is a transcription factor activated by a wide variety of agents, leading to cell activation, differentiation, or apoptosis. Reporter constructs utilizing the NF-kB promoter element are used to screen supernatants for such activity.

This gene is expressed primarily in synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,immune or musculoskeletal disorders, particularly synovial sarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.skeletal, immune, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:114 as residues: Cys-7 to Ser-13.

In addition, the expression of this gene product in synovium would suggest a role in the detection and treatment of disorders and conditions affecting the skeletal system, in particular osteoporosis as well as disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chrondomalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis,

lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, andspecific joint abnormalities as well as chondrodysplasias ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid. The detected NF-Kb biological activity in T-cells is consistent with the described uses for this protein. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:41 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 536 of SEQ ID NO:41, b is an integer of 15 to 550, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 32

The translation product of this gene shares sequence homology with the elastin like protein from Drosophila melanogaster which is believed to important in the maintainance of the extracellular matrix of tissues (See Genbank Accession No. gil762925). When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon-sensitive responsive element) pathway. Thus, it is likely that this gene activates leukemia cells through the Jaks-STAT signal transduction pathway. ISRE is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. The gene encoding the disclosed cDNA is believed to reside on chromosome 2. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 2.

This gene is expressed in synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,skeletal disorders, particularly synovial sarcoma. Similarly, polypeptides

and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, skeletal, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

In addition, the expression of this gene product in synovium, combined with its homology to elastin and ISRE activity, would suggest a role in the detection and treatment of disorders and conditions affecting the skeletal system, in particular osteoporosis as well as disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chrondomalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:42 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 588 of SEQ ID NO:42, b is an integer of 15 to 602, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 33

The translation product of this gene shares sequence homology with the cell division control protein CDC91 from the yeast, Saccharomyces cerevisiae.

This gene is expressed in testis, colon, and retina. It is also present in several cancerous tissues such as glioblastoma and Wilm's tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,cancers, including gliobalstoma and Wilm's tumor, in addition to reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, reproductive, gastrointestinal, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, seminal fluid, vitreous humor, aqueous humor, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:116 as residues: Arg-131 to Leu-136.

The tissue distribution and homology to a yeast cell division control protein CDC91, indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:43 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1613 of SEQ ID NO:43, b is an integer of 15 to 1627, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where b is greater than or equal to a + 14.

<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (39)
<223> Xaa equals stop translation

<400> 92
Met Ser Thr Val Lys Gln Ile Val Met Gly Leu Tyr Phe Val Tyr Xaa
1 5 10 15

Tyr Val Cys Phe Phe Tyr Ser Thr Phe Cys Gly Ser Ser Val Leu Leu
20 25 30

Val Ala Ser Ser Leu Leu Xaa
35

<210> 93
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (53)
<223> Xaa equals stop translation

<400> 93
Met Cys Leu Phe Phe Glu Asn Val Thr Leu Leu Phe Val Ile Val Leu
1 5 10 15

His Phe Ser Ala Phe Arg Pro Leu Tyr Phe His Lys Thr Pro Lys Thr
20 25 30

Ala Phe Asn Tyr Ile Ile Met Ser Val Phe Leu Asp Thr Asn Phe Cys
35 40 45

Ser Arg Met Thr Xaa
50

<210> 94
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (337)
<223> Xaa equals stop translation

any integer between 1 to 1443 of SEQ ID NO:44, b is an integer of 15 to 1457, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:44, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 35

The translation product of this gene shares sequence homology with the human ADAM 21 protein, a testis-specific metalloprotease-like which is thought to be important in egg recognition during fertilization, and possibly in a more general role in integrin-mediated cell-cell recognition, adhesion or signalling (See Genbank Accession No.gil2739137 (AF029900)). In specific embodiments, polypeptides of the invention comprise the sequence:
FCYLCILLLIVLFILLCCLYRLCKKSKPXKKQQXVQTPSAKEEEKIQRRPHELPP QSQPWVM PSQSQPPVTPSQSHPQVMPSQSQPPVTPSQSQPRVMPSQSQPPVM PSQSHPQLTPSQSQPPVTPSQRQPQ LMPSQSQPPVTPS (SEQ ID NO:181), IRHETECGIDHICIHRHCVHITILNSNCSPAFCNKRGICNNKHHCHCNYLWDPP NCLIKGYGGSVDSGPP P (SEQ ID NO:179), or GICNNKHHCHC (SEQ ID NO:180). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in human testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,reproductive disorders, particularly of the testis, or allergy, infectious and inflammatatory diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:118 as residues: Arg-12 to Ser-18.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system or reproductive disorders. The homology of this gene product to a

human metalloproteinase indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, the tissue distribution within testes, combined with its homology to a testes-specific metalloproteinase indicates that the protein product of this gene may shoe utility in the detection, treatment, and/or prevention of various reproductive disorders, particularly male infertility. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:45 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 874 of SEQ ID NO:45, b is an integer of 15 to 888, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

The translation product of this gene shares sequence homology with the human lysozyme which is thought to be important in the hydrolysis of proteins specific to bacteriolysis (See Genbank Accession No.P90343). As such the protein product of this gene may be useful as in antibiotic applications.

This gene is expressed primarily in testes and neutrophils induced by IL-1 and LPS.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to,immune disorders and afflications, particularly in bacteria infections, and reproductive disorders, such as male infertility. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:119 as residues: Lys-30 to Gly-35, Glu-64 to Gly-69.

The tissue distribution combined with the homology ot the human lysozyme protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders, particularly bacterial infections. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:46 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides

comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 738 of SEQ ID NO:46, b is an integer of 15 to 752, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:46, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

The translation product of this gene shares sequence homology with human ApoE4L1 protease which is thought to be important in Alzheimer's disease. When tested against PC12 cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) pathway. Thus, it is likely that this gene activates sensory neuron cells through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jaks-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation.

This gene is expressed primarily in small intestine, and to a lesser extent in T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,Alzheimer's disease, Downs syndrome, Parkinson's diseases and cardiovascular disease, or gastrointestinal or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, gastrointestinal, neural, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The homology to ApoE4L1 combined with the detected EGR1 activity indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the

gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the expression within the small intestine and T-cells, indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:47 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1774 of SEQ ID NO:47, b is an integer of 15 to 1788, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

This gene is expressed primarily in human adult testis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,reproductive or endocrine disorders, particularly male infertility. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male

reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.endocrine, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g.seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:121 as residues: Met-1 to Ser-10.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancrease (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-,hypoparathyroidism) , hypothallamus, and testes. Alternatively, expression within testes indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/ or prevention of a variety of male reproductive disorders, particularly male infertility. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:48 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 646 of SEQ ID NO:48, b is an integer of 15 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

The translation product of this gene shares sequence homology with ankyrin which is thought to be important in cell-cell interactions.

This gene is expressed in osteoblasts and tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include [illegible] are

not limited to,disorders affecting the skeletal or immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, skeletal, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:122 as residues: Lys-41 to Gln-46.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, expression within osteoblasts indicates a role in the detection and treatment of disorders and conditions affecting the skeletal system, in particular osteoporosis as well as disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chrondomalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly

available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:49 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1307 of SEQ ID NO:49, b is an integer of 15 to 1321, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:49, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 40

This gene is expressed in bone marrow, testes, liver, and retina.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,disorders affecting the immune, reproductive, or hepatic systems, such as AIDS, infertility, or cirrhosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, reproductive, hepatic, ocular, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, bile, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:123 as residues: Leu-20 to Pro-26.

The tissue distribution in liver indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). Alternatively, The secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological acitivities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human

immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:50 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 534 of SEQ ID NO:50, b is an integer of 15 to 548, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:50, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene is expressed primarily in T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,disorders affecting the immune or hematopoietic system, particularly immunodeficiencies such as AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the

standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:51 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 644 of SEQ ID NO:51, b is an integer of 15 to 658, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

This gene is expressed in the immune system, especially T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,disorders of the immune system, particularly immunodeficiencies such as AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:125 as residues: Thr-6 to Leu-11, Pro-13 to Cys-27, Pro-65 to Met-72.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:52 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 608 of SEQ ID NO:52, b is an integer of 15 to 622, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:52, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 43

This gene is expressed in T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,disorders of the immune system, particularly immunodeciencies such as AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:53 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly,

preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 709 of SEQ ID NO:53, b is an integer of 15 to 723, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:53, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

The translation product of this gene shares sequence homology with calmodulin which is known to be important in intracellular signalling.

This gene is expressed in T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,disorders of the immune system, particularly immunodeficienceis such as AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of

various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:54 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 894 of SEQ ID NO:54, b is an integer of 15 to 908, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:54, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 45

This gene is expressed primarily in the lung and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,cardiopulmonary or endocrine or reproductive disorders, including cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.cardiopulmonary, endocrine, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, treatment, or prevention of various lung and reproductive disorders, including cancer. Alternatively, expression within ovaries indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancrease (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g.,

hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-,hypoparathyroidism) , hypothallamus, and testes. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:55 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 808 of SEQ ID NO:55, b is an integer of 15 to 822, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:55, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 46

The translation product of this gene was shown to have homology to the human 150 kDa oxygen-regulated protein ORP150, which may be involved in metabolic processes (See Genbank Accession No. AA004278). In specific embodiments, polypeptides of the invention comprise the sequence: GSFRGTGRGRDGAQHPLLYVKLLIQVGHEPMPPTLGTNVLGRKVLYLPSFFTY AKYIVQVDGKIGLFRGLSPRLMSNALSTVTRGSMKKVFPPDEIEQVSNKDD MKTSLKKVVKETSYEMMMQCVSRMLAHPLHVIS MRCMVQFVGREAKY SGVLSSIGKIFKEEGLLGFFVGLIPHLLGDVVFLWGCNLLAHFINAYLVDDSVS DTPGGLGNDQNPGSQFSQALAIRSYTKFV (SEQ ID NO:182). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in the breast, brain, and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,disorders of the reproductive, neural, or hematopoietic system, including cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, skeletal, and central nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, neural, skeletal, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in brain tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, expression within the bone marrow indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the abovelisted tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:56 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1937 of SEQ ID NO:56, b is an integer of 15 to 1951, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:56, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 47

This gene is expressed primarily in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, developing, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:130 as residues: Ser-49 to Cys-54.

Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:57 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 649 of SEQ ID NO:57, b is an integer of 15 to 663, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

The gene encoding the disclosed cDNA is believed to reside on chromosome 18. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 18.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,disorders affecting the brain and central nervous system, particularly neurodegenerative disordes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:58 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is

any integer between 1 to 764 of SEQ ID NO:58, b is an integer of 15 to 778, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 49

The translation product of this gene shares sequence homology with pigment epithelium derived factor which is thought to be important in enhancing neuronal cell survival and inhibiting glial cell proliferation, useful, e.g. in CNS cell culture or to treat neuro-degenerative diseases.

This gene is expressed primarily in epithelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neural or integumentary disorders, particularly those affecting epithelial cells, such as cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neural, or integumentary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. epithelial, neural, integumentary, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in epithelium, combined with the homology to the PEDF protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e.wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chicken pox, molluscum contagiosum, herpes zoster, boils,

cellulitis, erysipelas, impetigo, tinea, althletes foot, and ringworm). Alternatively, the homology to the PDEF protein also indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:59 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 968 of SEQ ID NO:59, b is an integer of 15 to 982, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

This gene is expressed primarily in the ovary and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,disorders of the reproductive system, including developing tissue. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, developing, and cancerous and wounded tissues) or bodily fluids (e.g.amntiotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:133 as residues: Cys-43 to Lys-49.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of a variety of reproductive disorders, particularly infertility. In addition, expression within placental tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:60 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 392 of SEQ ID NO:60, b is an integer of 15 to 406, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 51

This gene is expressed primarily in immune cells, including B cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,immune disorders, particularly B cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and

spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:134 as residues: Thr-15 to Cys-21, Pro-60 to His-65, Pro-68 to Asp-74.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in B-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:61 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 799 of SEQ ID NO:61, b is an integer of 15 to 813, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:61, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 52

This gene is expressed primarily in pineal gland, epididymus, and to a lesser extent in bone marrow, melanocyte and cd34 positive cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to,endocrine, reproductive, or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, endocrine, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in pineal gland indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancrease (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-,hypoparathyroidism) , hypothallamus, and testes. Alternatively, the expression in a variety of immune and hematopoietic disordes indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or prolifcration of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:62 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides

comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 832 of SEQ ID NO:62, b is an integer of 15 to 846, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

When tested against U937 cell lines, supernatants removed from cells containing this gene activated the GAS (gamma activation site) promoter. Thus, it is likely that this gene activates promyelocyctic cells through the Jaks-STAT signal transduction pathway. GAS is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in frontal cortex and cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neural or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the

developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:63 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1428 of SEQ ID NO:63, b is an integer of 15 to 1442, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 54

This gene is expressed primarily in T-cell activated by PHA.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,immune disorders, particularly those imvolving T lymphocytes, such as immunodeficiency disorders and AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:137 as residues: Ser-17 to Met-22, Cys-25 to Thr-37.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product

may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:64 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 990 of SEQ ID NO:64, b is an integer of 15 to 1004, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 55

The translation product of this gene shares sequence homology with mouse transmembrane protein which is thought to be important in tumorigenesis (See Genbank Accession No. gil535682). In specific embodiments, polypeptides of the invention comprise the sequence:
ARAAPRLLLLFLVPLLWAPAAVRAGPDEDLSHRNKEPPAPAQQLQPQPVAVQG
PEPARVEDPYGVAVGGTVGHCLCTGLAVIGGRMIAQKISVRTVTIIGGIVFLA
FAFSALFISPDSGF (SEQ ID NO:183). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in skin tumor,colorectal tumor, placenta and synovial fibroblast and to a lesser extent in mutiple sclerosis, lymphoma, hypothalmus and spinal cord.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are

not limited to,integumentary disorders, particularly tumors, sclerosis, or reproductive or neural disorders, such as schizophrenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nueral and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.skeletal, reproductive, integumentary, neural, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:138 as residues: Gly-7 to Pro-15.

The tissue distribution combined with its homology to a putative tumorogenic protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within skin and colon tumors, in addition to placental tissue, and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Additionally, the expression in hematopoietic cells and tissues indicates that this protein may play a role in the proliferation, differentiation, and/or survival of hematopoietic cell lineages. In such an event, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoietic lineages from early hematopoietic stem and committed progenitor cells. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:65 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1669 of SEQ ID NO:65, b is an integer of 15 to 1683, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:65, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

The translation product of this gene was shown to have homology to the human hMed7 protein which is thought to play a pivotal role in regulation of the human RNA polymerase II C-terminal domain (See Genbank Accession No.gil2736290 (AF031383)). In specific embodiments, polypeptides of the invention comprise the sequence: FRIAWLLCLMICLIQKQECRVKTEPMDADDSNNCTGQNEHQRENSGHRRDQIIE KDAALCVLIDEMNERP (SEQ ID NO:184), RVKTEPMDADDSNNCTGQNEHQR ENSGHRRDQIIEKDAALCVLIDEMNERP (SEQ ID NO:185), QVSALPPPPMQYI KEYTDENIQEGLA (SEQ ID NO:186), SQGIERLHPMQFDHKKELRKLNMS (SEQ ID NO:187), or LETAERFQKHLERVIEMIQNCLASLPDDLPH (SEQ ID NO:188). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in fetal tissues, placenta, and various tumors. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,developmental disorders and tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.developmental, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution combined with the homology to the human hMed7 protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Additionally, the expression in hematopoietic cells and tissues indicates that this protein may play a role in the proliferation, differentiation, and/or survival of hematopoietic cell lineages. In such an event, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoietic lineages from early hematopoietic stem and committed progenitor cells

Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the abovelisted tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:66 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1427 of SEQ ID NO:66, b is an integer of 15 to 1441, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:66, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 57

This gene is expressed primarily in human early stage brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions:developmental or neural disorders, particularly maliganant fibrous histiocytoma and related cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, developmental, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism. and altered behaviors. including disorders in feeding, sleep

patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Additionally, the expression in hematopoietic cells and tissues indicates that this protein may play a role in the proliferation, differentiation, and/or survival of hematopoietic cell lineages. In such an event, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoietic lineages from early hematopoietic stem and committed progenitor cells. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the abovelisted tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:67 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 608 of SEQ ID NO:67, b is an integer of 15 to 622, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:67, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

The translation product of this gene was shown to have homology to an R47650 Interferon induced 1-8 gene encoded polypeptide which is known to be able to inhibit retroviral protein synthesis and/or assembly of retroviral structural proteins. The polypeptide can be used for treating or preventing retroviral infection, e.g. HIV; HTLV; bovine leukaemia virus, or can be used to assay the efficacy of interferon therapy. They can also be used for extracorporeal treatment of a host's cells or for inhibiting retroviral replication in the cell. In specific embodiments, polypeptides of the invention comprise the sequence: MTMITPSSKLTLTKGNKSWSSTAVAAALE LVDPPGCRNSPPPPH

TPFSYAFGVLDGNLGGERKDRSGLPQPLLLLSPRVRIAGAPPPSWFLRTRPFSF CLYLLRILSLLMWLTPLPPLPAGGWPGGQVPAGAVNRXCAFVLVCACAVFL CFDRS (SEQ ID NO:189), or LTLTKGNKSWSSTAVAAALELVDPPGCR (SEQ ID NO:190). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in eosinophils, fetal liver, and small intestine

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,hepatic, developmental, or immune disorders, particularly inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.hepatic, immune, developmental, gastrointestinal, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:141 as residues: Glu-12 to Gln-18.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in eosinophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, expression within infant liver indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of

liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). In addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various would-healing models and/or tissue trauma. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:68 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 602 of SEQ ID NO:68, b is an integer of 15 to 616, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:68, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

The gene encoding the disclosed cDNA is believed to reside on chromosome 8. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 8.

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neural or developmental disorders, particularly ischemic damage to the CNS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, developmental, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:142 as residues: Met-1 to Ser-6, Pro-51 to Ser-57, Ser-78 to Asp-93.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:69 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1005 of SEQ ID NO:69, b is an integer of 15 to 1019, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:69, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

The gene encoding the disclosed cDNA is believed to reside on chromosome 7. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 7.

This gene is expressed primarily in the immune system including T helper II cells, neutrophils, buffy coat and lymph nodes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,immune or hematopoietic disorders, particularly inflamation, autoimmunity, and immunodeficiencies such as AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell

types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:70 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 817 of SEQ ID NO:70, b is an integer of 15 to 831, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:70, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

This gene is expressed in the medulla region of Kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are

not limited to,urogenital or renal disorders, particularly kidney failure. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.urogenital, renal, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:144 as residues: Lys-8 to Thr-13, Glu-39 to Gly-46.

The tissue distribution in kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:71 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 736 of SEQ ID NO:71, b is an integer of 15 to 750, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 62

This gene is expressed primarily in a prostate cells and testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to reproductive disorders, particularly prostatic hyperplasia, prostatic cancer

and testes cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, urogenital, endocrine, and cancerous and wounded tissues) or bodily fluids (e.g.seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:145 as residues: Lys-19 to Asn-32.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various disorders of the reproductive system, including cancers of the prostate or testes. Alternatively, the expression within testes may suggest that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancrease (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-,hypoparathyroidism) , hypothallamus, and testes. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:72 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 700 of SEQ ID NO:72, b is an integer of 15 to 714, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:72, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

This gene is expressed primarily in hepatocellular tumors, skin tumors, osteoclastoma, and to a lesser extent in kidney and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,tumors particularly of the hepatic, inegumentary or skeletal system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skin and hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.integumentary, hepatic, skeletal, urogenital, endocrine, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:146 as residues: Pro-10 to Pro-17.

The tissue distribution in skin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e.wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, althletes foot, and ringworm). Alternatively, expression within bone would suggest a role in the detection and treatment of disorders and conditions affecting the skeletal system, in particular osteoporosis as well as disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chrondomalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). Protein, as well as, antibodies directed against the

protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:73 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1391 of SEQ ID NO:73, b is an integer of 15 to 1405, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:73, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

This gene is expressed primarily in meningima.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,meningioma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Central Nervous System, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.neural, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating tumors of the meninges. Similarly, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo,

sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:74 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 893 of SEQ ID NO:74, b is an integer of 15 to 907, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:74, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in Wilm's tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,urogenital or renal disorders, particularly tumors of the kidney. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.renal, urogenital, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:148 as residues: Glu-6 to Cys-12.

The tissue distribution in kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility

as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:75 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 673 of SEQ ID NO:75, b is an integer of 15 to 687, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,immune or hematopoietic disorders, such as autoimmune disease or inflammatory disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore, it may be also

used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:76 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 778 of SEQ ID NO:76, b is an integer of 15 to 792, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,immune or hematopoietic disorders, such as diseases resulting from chronic or acute inflammatory response. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:150 as residues: Pro-43 to Ser-49, Met-56 to Gly-66, Gln-69 to Pro-75.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:77 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 742 of SEQ ID NO:77, b is an integer of 15 to 756, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 68

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,immune or hematopoietic disorders, such as inflammation or autoimmune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic system, expression of this gene at significantly higher or lower levels may

be routinely detected in certain tissues or cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:151 as residues: Pro-24 to Glu-29, Glu-31 to Pro-37, Pro-48 to Asp-55, Arg-87 to Pro-93, Pro-100 to Ser-106.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:78 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 737 of SEQ ID NO:78, b is an integer of 15 to 751, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

The gene encoding the disclosed cDNA is believed to reside on chromosome 12. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 12.

This gene is expressed primarily in the fetal ear, and to a lesser extent, in osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,skeletal or developmental disorders, particularly abnormal bone formation such as bone tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.skeletal, epithelial, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

In addition, the expression of this gene product in osteoclasts would suggest a role in the detection and treatment of disorders and conditions affecting the skeletal system, in particular osteoporosis as well as disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chrondomalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:79 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of

a-b, where a is any integer between 1 to 1397 of SEQ ID NO:79, b is an integer of 15 to 1411, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:79, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 70

The translation product of this gene was found to have homology to the human kidney epidermal growth factor precursor (See Genbank Accession No. R51437). The gene encoding the disclosed cDNA is believed to reside on chromosome 3. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 3.

This gene is expressed primarily in brain, and to a lesser extent, in prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,neural or reproductive disorders, particularly prostate disease such as tumors of the prostate and benign prostatic hypertrophy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine, neural or reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, neural, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:153 as residues: Ser-49 to Arg-54.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, expression within the prostate indicates that the translation

product of this gene is useful for the detection, treatment, and/or prevention of a variety of reproductive disorders, including prostate cancer, and infertility.Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:80 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 852 of SEQ ID NO:80, b is an integer of 15 to 866, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:80, and where b is greater than or equal to a + 14.

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
1	HCUDK80	209178 07/24/97	ZAP Express	11	392	1	392	80	80	84	1	26	27	29
2	HCWFV11	209178 07/24/97	ZAP Express	12	465	1	465	126	126	85	1	33	34	33
3	HCWHN10	209178 07/24/97	ZAP Express	13	674	1	674	85	85	86	1	25	26	65
4	HCWHT35	209178 07/24/97	ZAP Express	14	297	1	297	36	36	87	1	16	17	26
5	HDTAE40	209178 07/24/97	pCMVSport 2.0	15	604	1	604	110	110	88	1	34	35	48
6	HE2BX71	209178 07/24/97	Uni-ZAP XR	16	1146	203	1146	276	276	89	1	27	28	32
7	HE2EO70	209178 07/24/97	Uni-ZAP XR	17	678	1	678	150	150	90	1	15	16	22

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
8	HE8DY08	209178 07/24/97	Uni-ZAP XR	18	1305	393	1305	734	734	91	1	23	24	54
9	HE9NB19	209178 07/24/97	Uni-ZAP XR	19	1060	1	1060	174	174	92	1	26	27	38
10	HE9ND27	209178 07/24/97	Uni-ZAP XR	20	1170	95	1170	353	353	93	1	27	28	52
11	HCE3G69	209878 05/18/98	Uni-ZAP XR	21	2084	1	2084	165	165	94	1	19	20	336
11	HEAAA85	209178 07/24/97	Uni-ZAP XR	81	2078	1290	2065	1295	1295	154	1	58	59	118
12	HEAAX57	209178 07/24/97	Uni-ZAP XR	22	643	1	643	127	127	95	1	38	39	48
13	HEEAG93	209178 07/24/97	Uni-ZAP XR	23	647	1	647	334	334	96	1	21	22	37
14	HEGAI91	209178 07/24/97	Uni-ZAP XR	24	825	1	825	179	179	97	1	18	19	28

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
15	HEIAU93	209178 07/24/97	Uni-ZAP XR	25	541	1	541	96	96	98	1	24	25	35
16	HEMGD15	209178 07/24/97	Uni-ZAP XR	26	852	1	711	20	20	99	1	31	32	181
17	HEQBR95	209178 07/24/97	pCMVSport 3.0	27	4598	2673	3242	2767	2767	100	1	50	51	83
18	HFCEW42	209178 07/24/97	Uni-ZAP XR	28	585	1	585	95	95	101	1	18	19	24
19	HFIXC91	209178 07/24/97	pSport1	29	824	1	824	244	244	102	1	19	20	31
20	HFKFN45	209178 07/24/97	Uni-ZAP XR	30	773	153	721	428	428	103	1	25	26	27
21	HFKGE44	209178 07/24/97	Uni-ZAP XR	31	969	141	969	363	363	104	1	29	30	86
22	HFPCY39	209178 07/24/97	Uni-ZAP XR	32	1355	1	606	362	362	105	1	14	15	127

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5" NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
23	HFTBS49	209178 07/24/97	Uni-ZAP XR	33	536	1	362	232	232	106	1	30	31	30
24	HFVHE58	209178 07/24/97	pBluescript	34	1123	594	1123	762	762	107	1	17	18	31
25	HFXDX75	209178 07/24/97	Lambda ZAP II	35	587	1	587	300	300	108	1	29	30	96
26	HFXFZ81	209178 07/24/97	Lambda ZAP II	36	842	1	842	129	129	109	1	16	17	21
27	HFXJC53	209178 07/24/97	Lambda ZAP II	37	953	1	953	707	707	110	1	42	43	46
28	HFXJW48	209178 07/24/97	Lambda ZAP II	38	2211	63	635	356	356	111	1	17	18	355
29	HGBGO11	209178 07/24/97	Uni-ZAP XR	39	682	1	682	58	58	112	1	36	37	70
30	HGBHM10	209178 07/24/97	Uni-ZAP XR	40	685	18	665	36	36	113	1	17	18	170

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
31	HSSAO72	209194 08/01/97	Uni-ZAP XR	41	550	1	550	28	28	114	1	34	35	35
32	HSSEO83	209194 08/01/97	Uni-ZAP XR	42	602	1	602	233	233	115	1			13
33	HSWAY58	209194 08/01/97	pCMVSport 3.0	43	1627	702	1627	815	815	116	1	18	19	155
34	HSXAR64	209194 08/01/97	Uni-ZAP XR	44	1457	1000	1457	1191	1191	117	1	24	25	38
35	HTECE72	209194 08/01/97	Uni-ZAP XR	45	888	1	888	184	184	118	1	46	47	45
36	HTEIM65	209194 08/01/97	Uni-ZAP XR	46	752	1	752	109	109	119	1	19	20	146
37	HTHBX95	209194 08/01/97	Uni-ZAP XR	47	1788	1025	1788	1054	1054	120	1	25	26	43
38	HTLDQ56	209194 08/01/97	Uni-ZAP XR	48	660	1	660	174	174	121	1	36	37	80

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
39	HTOFU06	209194 08/01/97	Uni-ZAP XR	49	1321	300	1321	255	255	122	1	16	17	98
39	HTOFU06	209194 08/01/97	Uni-ZAP XR	82	1064	15	1064	227	227	155	1	27	28	27
40	HTPDX06	209194 08/01/97	Uni-ZAP XR	50	548	1	548	216	216	123	1	21	22	31
41	HTWCE16	209194 08/01/97	pSport1	51	658	1	658	208	208	124	1	19	20	21
42	HTWEE31	209194 08/01/97	pSport1	52	622	1	622	27	27	125	1	41	42	121
43	HTWEL91	209194 08/01/97	pSport1	53	723	1	723	154	154	126	1	23	24	25
44	HTXDE07	209194 08/01/97	Uni-ZAP XR	54	908	1	908	84	84	127	1			23
45	HUFBO40	209194 08/01/97	pSport1	55	822	1	816	172	172	128	1	24	25	38

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
46	HUSAO56	209194 08/01/97	Lambda ZAP II	56	1951	839	1947	922	922	129	1	26	27	73
47	HUSIJ08	209194 08/01/97	pSport1	57	663	1	663	351	351	130	1	50	51	54
48	HAGBD57	209194 08/01/97	Uni-ZAP XR	58	778	1	778	221	221	131	1	29	30	43
49	HAICJ56	209194 08/01/97	Uni-ZAP XR	59	982	1	982	68	68	132	1	24	25	36
50	HBAFA04	209194 08/01/97	pSport1	60	406	1	406	96	96	133	1	33	34	49
51	HBJES16	209194 08/01/97	Uni-ZAP XR	61	813	1	813	309	309	134	1	56	57	84
52	HBMTA15	209194 08/01/97	Uni-ZAP XR	62	846	1	846	116	116	135	1	19	20	22
53	HCEFZ05	209194 08/01/97	Uni-ZAP XR	63	1442	548	1442	587	587	136	1	15	16	44

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
54	HCFMX95	209194 08/01/97	pSport1	64	1004	1	1004	186	186	137	1	16	17	46
55	HLYHA71	209852 05/07/98	pSport1	65	1683	156	1683	55	55	138	1	25	26	288
55	HDTAR09	209194 08/01/97	pCMVSport 2.0	83	1126	355	1126	-602	602	156	1	15	16	45
56	HE9FC17	209194 08/01/97	Uni-ZAP XR	66	1441	590	1087	780	780	139	1	17	18	23
57	HEBAL06	209194 08/01/97	Uni-ZAP XR	67	622	1	622	93	93	140	1	18	19	53
58	HEIAB33	209195 08/01/97	Uni-ZAP XR	68	616	1	616	269	269	141	1	43	44	60
59	HEPBC02	209195 08/01/97	Uni-ZAP XR	69	1019	15	829	137	137	142	1	36	37	100
60	HFTBY96	209195 08/01/97	Uni-ZAP XR	70	831	1	831	150	150	143	1	17	18	41

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
61	HKMMM61	209195 08/01/97	pBluescript	71	750	1	750	130	130	144	1	37	38	62
62	HL3AA35	209195 08/01/97	Uni-ZAP XR	72	714	1	714	56	56	145	1	24	25	32
63	HLQBQ38	209195 08/01/97	Lambda ZAP II	73	1405	453	1405	472	472	146	1	39	40	41
64	HMKCP66	209195 08/01/97	pSport1	74	907	1	907	353	353	147	1	19	20	40
65	HWTAL40	209195 08/01/97	Uni-ZAP XR	75	687	51	687	124	124	148	1	31	32	43
66	HNHDR03	209195 08/01/97	Uni-ZAP XR	76	792	1	792	184	184	149	1	45	46	54
67	HNHFH41	209195 08/01/97	Uni-ZAP XR	77	756	1	756	52	52	150	1	24	25	165
68	HNHFI81	209195 08/01/97	Uni-ZAP XR	78	751	1	751	46	46	151	1	18	19	113

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
69	HOSFQ28	209195 08/01/97	Uni-ZAP XR	79	1411	219	987	304	304	152	1	20	21	39
70	HPRAL78	209195 08/01/97	Uni-ZAP XR	80	866	128	866	148	148	153	1	42	43	63

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly , the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification , such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, Virus Res. 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, Nucleic Acids Res. 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, supra.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., Protein Engineering 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., + or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Polynucleotide and Polypeptide Variants

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown inTable 1, the ORF (open reading frame), or any fragement specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the presence invention can be determined conventionally using known computer programs. A preferred method for determing the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identiy are:
Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization

Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the lenght of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is becuase the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignement of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequnce are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query

amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be determined conventionally using known computer programs. A preferred method for determing the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is becuase the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequnce are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as E. coli).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988 (1993) reported variant KGF proteins having heparin binding activity even after

deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity. More preferably, these polynucleotides can be used as probes or primers as discussed herein.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-

60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')2 fragments) which are capable of specifically binding to protein. Fab and F(ab')2 fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the

polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat

polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library).) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined.

First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identi

personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses f the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, 131I, 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of 99mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the

proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitis, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect

interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstron's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes

Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiollitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox , hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Menigococcal), Pasteurellacea Infections (e.g., Actinobacillus, Heamophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue

regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stoke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

Chemotaxis

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotaxic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotaxic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotaxic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors),or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity , and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, caricadic rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of

positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which [illegible]es a human cDNA clone identified by a cDNA Clone Identifier in Table 1, [illegible] molecule is contained in the material deposited with the American Type

Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not in ended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

Vector Used to Construct Library	Corresponding Deposited Plasmid
Lambda Zap	pBluescript (pBS)
Uni-Zap XR	pBluescript (pBS)
Zap Express	pBK
lafmid BA	plafmid BA
pSport1	pSport1
pCMVSport 2.0	pCMVSport 2.0
pCMVSport 3.0	pCMVSport 3.0
pCR®2.1	pCR®2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain

DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR®2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM $MgCl_2$, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is

used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P^{32} using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on

either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 ($O.D.^{600}$) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high

affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM immidazole. Immidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4° C or frozen at -80° C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

The following alternative method can be used to purify a polypeptide expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem

columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak Drosophila promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., Virology 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring

signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five µg of a plasmid containing the polynucleotide is co-transfected with 1.0 µg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One µg of BaculoGold™ virus DNA and 5 µg of the plasmid are mixed in a sterile well of a microtiter plate containing 50 µl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 µl Lipofectin plus 90 µl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture

and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 µCi of ^{35}S-methionine and 5 µCi ^{35}S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSport 2.0, and pCMVSport 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No.209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five µg of the expression plasmid pC6 is cotransfected with 0.5 µg of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of metothrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 µM, 2 µM, 5 µM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 µM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCCAAAACC
CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA
GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of present invention is administered to an animal to induce the production of sera

containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')2 and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2 x 10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced [illegible] described in

Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl2 (anhyd); 0.00130 mg/L $CuSO_4$-$5H_2O$; 0.050 mg/L of $Fe(NO_3)_3$-$9H_2O$; 0.417 mg/L of $FeSO_4$-$7H_2O$; 311.80 mg/L of Kcl; 28.64 mg/L of $MgCl_2$; 48.84 mg/L of $MgSO_4$; 6995.50 mg/L of NaCl; 2400.0 mg/L of $NaHCO_3$; 62.50 mg/L of NaH_2PO_4-H_2O; 71.02 mg/L of Na_2HPO4; .4320 mg/L of $ZnSO_4$-$7H_2O$; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H_2O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H_2O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H_2O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalainine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tryrosine-2Na-$2H_2O$; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 m[illegible] Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B_{12}[illegible] of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine;

0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proxial region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

Ligand	JAKs tyk2	Jak1	Jak2	Jak3	STATS	GAS(elements) or ISRE
IFN family						
IFN-a/B	+	+	-	-	1,2,3	ISRE
IFN-g		+	+	-	1	GAS (IRF1>Lys6>IFP)
Il-10	+	?	?	-	1,3	
gp130 family						
IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS (IRF1>Lys6>IFP)
Il-11(Pleiotrohic)	?	+	?	?	1,3	
OnM(Pleiotrohic)	?	+	+	?	1,3	
LIF(Pleiotrohic)	?	+	+	?	1,3	
CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
G-CSF(Pleiotrohic)	?	+	?	?	1,3	
IL-12(Pleiotrohic)	+	-	+	+	1,3	
g-C family						
IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP >>Ly6)(IgH)
IL-7 (lymphocytes)	-	+	-	+	5	GAS
IL-9 (lymphocytes)	-	+	-	+	5	GAS
IL-13 (lymphocyte)	-	+	?	?	6	GAS
IL-15	?	+	?	+	5	GAS
gp140 family						
IL-3 (myeloid)	-	-	+	-	5	GAS (IRF1>IFP>>Ly6)
IL-5 (myeloid)	-	-	+	-	5	GAS
GM-CSF (myeloid)	-	-	+	-	5	GAS
Growth hormone family						
GH	?	-	+	-	5	
PRL	?	+/-	+	-	1,3,5	
EPO	?	-	+	-	5	GAS(B-CAS>IRF1=IFP>>Ly6)
Receptor Tyrosine Kinases						
EGF	?	+	+	-	1,3	GAS (IRF1)
PDGF	?	+	+	-	1,3	
CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5':GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCG AAATGATTTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5':CTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAATG ATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC CTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGC CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGC CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT TGCAAAAAGCTT:3' (SEQ ID NO:5)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and, as is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, Il-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml genticin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI [illegible] serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final concentration of 10^7 cells/ml. Then add 1ml of 1 x 10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells. Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest $2x10e^7$ U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $Na_2HPO_4.7H_2O$, 1 mM $MgCl_2$, and 675 uM $CaCl_2$. Incubate at 37°C for 45 min.

Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

These cells are tested by harvesting $1x10^8$ cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of $5x10^5$ cells/ml. Plate 200 ul cells per well in the 96-well plate (or $1x10^5$ cells/well).

Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced by various tissues and cell types upon

activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS

(Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as $5x10^5$ cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to $1x10^5$ cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

NF-κB (Nuclear Factor κB) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF-κB regulates the expression of genes involved in immune cell activation, control of apoptosis (NF-κB appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κB is retained in the cytoplasm with I-κB (Inhibitor κB). However, upon stimulation, I- κB is phosphorylated and degraded, causing NF- κB to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κB include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF-κB promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF-kB would be useful in treating diseases. For example, inhibitors of NF-κB could be used to treat those diseases related to the acute or chronic activation of NF-kB, such as rheumatoid arthritis.

To construct a vector containing the NF-κB promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF-κB binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:

5' :GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5' :GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5' :CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCA TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTC CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT: 3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF-κB/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF-κB/SV40/SEAP cassette is removed from the above NF-κB/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF-κB/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF-κB/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat cells is also described

in Example 13. As a positive control, exogenous TNF alpha (0.1,1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 µl of 2.5x dilution buffer into Optiplates containing 35 µl of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 µl Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 µl Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
[illegible]	130	6.5
[illegible]	135	6.75
[illegible]	140	7
[illegible]	145	7.25

28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO_2 incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is

incubated at 37°C in a CO_2 incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10^6 cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10^6 cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca^{++} concentration.

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating

tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford,MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford,MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na3VO4, 2 mM Na4P2O7 and a cocktail of protease inhibitors (# 1836170) obtained from Boeheringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and

PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg_{2+} (5mM ATP/50mM $MgCl_2$), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM $MgCl_2$, 5 mM $MnCl_2$, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30°C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mm EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavadin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phospotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR

products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Manheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 µg/kg/hour to about 50 µg/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracistemally, intravaginally,

intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), bucally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or mirocapsules. Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other

disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties.

5

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 94, line N/A

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution
American Type Culture Collection

Address of depositary institution (*including postal code and country*)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
July 24, 1997	209178

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later (*specify the general nature of the indications, e.g., "Accession Number of Deposit"*)

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179

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 95, line N/A

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet

Name of depositary institution
American Type Culture Collection

Address of depositary institution (*including postal code and country*)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
May 18, 1998	209878

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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PAUL F. URRUTIA

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 98, line N/A

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet

Name of depositary institution
American Type Culture Collection

Address of depositary institution (*including postal code and country*)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
August 1, 1997	209194

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet

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181

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 101, line N/A

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution
American Type Culture Collection

Address of depositary institution (*including postal code and country*)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
May 7, 1998	209852

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 101, line N/A

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution
American Type Culture Collection

Address of depositary institution (*including postal code and country*)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
August 1, 1997	209195

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later (*specify the general nature of the indications, e.g., "Accession Number of Deposit"*)

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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

(f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence

identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(g) a variant of SEQ ID NO:Y;

(h) an allelic variant of SEQ ID NO:Y; or

(i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15. A method of making an isolated polypeptide comprising:

(a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and

(b) recovering said polypeptide.

16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

(a) contacting the polypeptide of claim 11 with a binding partner; and

(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

(a) expressing SEQ ID NO:X in a cell;

(b) isolating the supernatant;

(c) detecting an activity in a biological assay; and

(d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/17044

A. CLASSIFICATI N OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.
US CL :Please See Extra Sheet.
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 436/501; 435/320.1, 69.1, 6, 253.3; 530/350, 24, 387.1; 536/23.1, 23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	ADAMS et al, Complementary DNA sequencing: Expressed sequence tags and human genome project, Science, 21 June 1991, Vol. 252, pages 1651-1656, see entire document.	1-22

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 19 OCTOBER 1998	Date of mailing of the international search report 29 OCT 1998
Name and mailing address Commissioner of Patents Box PCT Washington, D.C. 20231 Facsimile No. (703)	Authorized officer JAMES MARTINELL Telephone No. (703) 308-0196

Form PCT/ISA/210

INTERNATIONAL SEARCH REP RT

International application No.
PCT/US98/17044

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 23
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

Claim 23 is directed to a product of the process of claim 22. Claim 22 is not a process for the production of a product, but a process for the detection of a substance. Hence, no meaningful search can be carried out.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/17044

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

C12N 15/11, 15/63, 15/00, 15/12; A61K 38/17; C07K 16/00; C12P 21/02; C12Q 1/68; G01N 33/68

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

436/501; 435/320.1, 69.1, 6, 253.3; 530/350, 24, 387.1; 536/23.1, 23.5

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

APS, STN, MPSRCH (SEQ Nos 11 and 84 only). One nucleotide sequence and one amino acid sequence have been searched. It is not clear which sequences are embraced by the claims because the claims refer to sequences X and Y. The table at pages 94-103 contains many sequences X and Y, yet the claims refer to X and Y in the singular only. If the claims are to embrace more than one X and more than one Y, it is not clear whether each X always requires the corresponding sequence Y (e.g., see claim 1(c)). Additionally, the claims are in improper format in referring to the description (see PCT Rule 6.2(a)). Accordingly, the first X nucleotide sequence disclosed and the first Y amino acid sequence disclosed were searched.

<110> Human Genome Sciences, Inc. et al.

<120> 70 Human Secreted Proteins

<130> PZ014.PCT

<140> PCT/US98/17044
<141> 1998-08-18

<150> 60/089,510
<151> 1998-06-16

<150> 60/092,956
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<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> Site
<222> (3)
<223> Xaa equals any of the twenty naturally ocurring L-amino acids

<400> 2
Trp Ser Xaa Trp Ser
1 5

<210> 3
<211> 86
<212> DNA
<213> Homo sapiens

<400> 3
gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60
cccgaaatat ctgccatctc aattag 86

<210> 4
<211> 27
<212> DNA
<213> Homo sapiens

<400> 4
gcggcaagct ttttgcaaag cctaggc 27

<210> 5
<211> 271
<212> DNA
<213> Homo sapiens

<400> 5
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60
aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 120
gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240
ttttggaggc ctaggctttt gcaaaaagct t 271

<210> 6
<211> 32
<212> DNA

<213> Homo sapiens

<400> 6
gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 7
<211> 31
<212> DNA
<213> Homo sapiens

<400> 7
gcgaagcttc gcgactcccc ggatccgcct c 31

<210> 8
<211> 12
<212> DNA
<213> Homo sapiens

<400> 8
ggggactttc cc 12

<210> 9
<211> 73
<212> DNA
<213> Homo sapiens

<400> 9
gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg 60
ccatctcaat tag 73

<210> 10
<211> 256
<212> DNA
<213> Homo sapiens

<400> 10
ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct 60
caattagtca gcaaccatag tcccgccccc aactccgccc atcccgcccc taactccgcc 120
cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180
ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggctttttg gaggcctagg 240
cttttgcaaa aagctt 256

<210> 11
<211> 392
<212> DNA
<213> Homo sapiens

<400> 11
gaattcggca cgagcgctgt tgggtgtgtg tatgtttgcg ctgggcgcgc ttgccgtgcc 60
ggtgaccggt ttcggcagta tgcctgcgct ctcgatggcg ctgaccatgc tcggctgcta 120
cgcgatagcc atcctgctgt tcgtgacgct ggtgcgcaaa ccggcttaac gttacttgat 180
gacagacagg caaaaaaaaa cccgcttcgg cggkttttt aagaattcgg ytaaagtcag 240
atagcgataa cgttagcagc cgacgggcct ttggcaccat tggtgatttc gaactctacg 300

cgctggcctt cagcgagggt cttgaagccc tggctggaaa tagcagagaa atgaacgaaa 360
acatctttgc tgccatcttc aggggtaatg aa 392

<210> 12
<211> 465
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (357)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (395)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (440)
<223> n equals a,t,g, or c

<400> 12
gaattcggca cgagctcact tgaaatccat gacactacat agaaaatgga ctctaaaatc 60
tgcctggcaa tgattctaca tttccctaat cccttcactt tcctactctc ccctactctc 120
ttagaatgtt ctgtatctcc ttatctttct tcaatctccc tgaatattct ccctgttcct 180
tgctttcagt tcaggaattg gtgccccaat ttttttatgt tgtttgattt ttttttttt 240
tttgagacag agtctggctc tgtcactggg gctggagtgc agtggtgcaa tcatggctca 300
ctgcaatctc tgcctcccag gctcgagagt attctagagc ggccgcgggc ccatcgnttt 360
tccaaccggg tggggtacca ggtaagtgta acccnattcg gcctatagtg agtccgtaat 420
taaaattcaa ctgggcggtn ggtttaaaaa cgtccgtgga actgg 465

<210> 13
<211> 674
<212> DNA
<213> Homo sapiens

<400> 13
tgcccctgaa gagtaagaat gaatatgaca tgttgattct tgaagtggcc aaataaatca 60
cccgacggtg aagttctgca atggatgaag gtggcagtga gaggaaagca gagagaatgc 120
agagacagga tcctaggcaa gaagacaaag gcctggacac agagaaggag atcaaagtgt 180
ggctctgggt acaaagtgag agtgagtgtg caggaagtga acaaggtcag tagaactagg 240
aaaagcmaaa ggtcaaggaa accagcattt ggagacagrt aatgatgtca cctttggacc 300
aagggagatt gaagcttctg taaggcraaa gtaaatgttc ctggttagta atccaggttc 360
ttggtaattg gtattaagtt tgtcatgtgc tgtggctcat gccaagtcca tccatataaa 420
gacaaccatg ttmgaataag aaagacaaag aactctcaga gtctgttcct gagatagagc 480
aggtcctgag aggcttatca aaagttcaga aactaaggca aaattttggc catgatattc 540
acaaaattga agagaaacag catttaataa tacagccaag cataaaaaaa accaagacaa 600
cctaaaaccc caatgccatt tgtattgaag gtgagtgggg agctcaccgg tggtctcaag 660
aacttggcag atgc 674

<210> 14
<211> 297
<212> DNA

<213> Homo sapiens

<400> 14
gaattcggca caggtctaaa tgagatggca cgggtatgct tctgttcttt ttctggacgt 60
tgtttagaga gtcagtagat cataataatt cagacacttt tttttckgga ccataaaata 120
tctgarscca yataataaca aacatacagc acggtgaata agaacccaac ttttgagcca 180
gatcactttg catggaatcc ccattctatc attctatcat ttctgggctg tgggaacctc 240
agacaagtta cttaacttct tcaatgctca gattaaaaaa aaaaaaaaaa aactcga 297

<210> 15
<211> 604
<212> DNA
<213> Homo sapiens

<400> 15
tcgacccacg cgtccgcagg gaaggaccct ttaagaggac atttactaaa atgcactttg 60
caacattaaa aagaagaccc tggaatacat ttctctcctt ctaagtgaaa tgctctcaaa 120
gagctctaag atggtgtcag ttaaacgggc tgacccgggg tctctgggtt tcactttctt 180
gctgtcctcc cttcccaagt gtacagtggg ggtctccaga ggccgcccca catgcaccag 240
ctgctctgat ggctgagata acgtctggca ttcccgttct tcaaattaaa cagaaacact 300
attcagtgtt ttcggtttta attaagaata cggtaaatat cagtcaatac agcccacatg 360
aacatggacc cctttggggt cctcaatgac ttcagaagtg attagtgctg aggtcagaaa 420
accggaggac aaaatcaatt acacgtcctg acaaggagct gagcctggca tcaactcaga 480
gaaggggttt gcagataaca gcattcacct gaggttccac taacacggaa taaagctgtg 540
gtataaaata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc 600
ggcc 604

<210> 16
<211> 1146
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (1140)
<223> n equals a,t,g, or c

<400> 16
cttaattatt aataagccaa tgtgttatga taccaatayc tgttttaaaa aactaaaacc 60
aaccatgctt ctggcatgat aaaatcatgg aattaaatca ggggtttaca ttcttgtaga 120
gtgttcttga aacactctct gcaccatttt taaaacttga gaatagtttt agtatctctg 180
atatttttg ccagaatcat catgtcatgt atgaatgtgt tatccctatc taaggaaaaa 240
ggtgaatatg tttttgtatg aatgtttaac tggaaatgtc catggacttg gctaatttat 300
atttactttt tattgtacat agatttctaa tatttttcat tcctgtatca tttaaacttc 360
cttcatttga gtaaattcac taaatatttc tatttttgc ttttttaaat tctgatttta 420
tatgaattct aattcttttt cactacatat gttttaaaga gttacataca gtgatttaga 480
atggtttaca gttaatgctg atcttgtatt ttaaattcca acactttgtg tcactacctc 540
ctctaatggt tagtatgata tgctagcaga ctgtatgagg tctttttttа aaataccact 600
tttagtgtca gtgaaccaaa ttctggaatg tcttaacagc tctaaatctt acttgtcttg 660
aaaatgattg gggtttaata ccactgctgg tggttcacac atcatcccat ccttaatatg 720
cctgacaggc atctgagcaa aggtttttag taattgaatt tctctgcagt agtccttcaa 780
gcacttgaat gtaaacattt agcatttatt cgtttaatga ctactgatac gaatctcaag 840
cagatttctt gc[illegible]ttatgtttc actgagttct ggttttgtgt agctatattt 900
tatatagcta ga[illegible]cagtgaaca tgaattgtaa taattggtta tttccttaag 960
tctttagatt at[illegible]agattattg cacgtctgtg atttgagagg tgagttattt 1020
aagaggc[illegible]tgaattt gaattgtaaa cctgttatct ctgtgaaact 1080

tttaacatga taaaatataa cctttctttg tgcttaaaaa aaaaaaaaaa aaaaaactcn 1140
aagggg 1146

<210> 17
<211> 678
<212> DNA
<213> Homo sapiens

<400> 17
ggcacgaggc ggaggtggag acgcagagct atatttggta gactgtgaac agactcacct 60
gcctagagca gtgtattcac attgggatta ttagagtaaa gtgtggacaa gaggtataat 120
gcagaggtct taatgtgtca ggctggggaa tgtacttagt attctgtctc tcatgtgtct 180
caaaccaggg tcctcattca cctgttggta cttggtgaca aggataaaaa agctcctccc 240
tactctgcta gttttacttc aaataatgaa gggaaactta taattaattg ataagtcatg 300
ttaaatatct ctgtagcaac ttaaatagga aatatgatgc tgaatttttct tgaattctta 360
aaataaggga tttccaaata atttgaagtt attactgctc ttttgagatt gttttcaaac 420
tctgacaatc actgatcatt ctctctgcct ttggaattct tgagagacaa agtgtggtta 480
tcacataagt attagggagt cattacaggt tgatgcatag aggaagagag agccacgttt 540
ctaataacac tcatacctga aatcattcca ttaccattct ttaatagttt cattctgact 600
tcattgtagc aactcttact ttattcttct taagttttta aggccaaatc atggtttcat 660
aaaaaaaaaa aaaaaaaa 678

<210> 18
<211> 1305
<212> DNA
<213> Homo sapiens

<400> 18
cagcttgtgc agactccgag ccttcagtga caaaggcttt gctgtttgtc ctcttgacct 60
gtgtctgact tgctcctgga tgggcaccca cactcagagg ctacatatgg ccctagagca 120
ccaccttcct ctagggacac tggggctacc tacagacaac ttcatctaag tcctaactat 180
tacaatgatg gactcagcac ctccaaagca gttaattttt cactagaacc agtgagatct 240
ggaggaatgt gagaagcata tgctaaatgt acattttaat tttagactac ttgaaaaggc 300
ccctaataag gctagaggtc taagtccccc acccctttcc ccactcccct ctagtggtga 360
actttagagg aaaaggaagt aattgcacaa ggagtttgat tcttaccttt tctcagttac 420
agaggacatt aactggatca ttgcttcccc agggcaggag agcgcagagc tagggaaagt 480
gaaaggtaat gaagatggag cagaatgagc agatgcagat caccagcaaa gtgcactgat 540
gtgtgagctc ttaagaccac tcagcatgac gactgagtag acttgtttac atctgatcaa 600
agcactgggc ttgtccaggc tcataataaa tgctccattg aatctactat tcttgttttc 660
cactgctgtg gaaacctcct tgctactata gcgtcttatg tatggtttaa aggaaattta 720
tcaggtgaga gagatgagca acgttgtctt ttctctcaaa gctgtaatgt gggttttgtt 780
ttactgttta tttgtttgtt gttgtatcct tttctccttg ttatttgccc ttcagaatgc 840
acttgggaaa ggctggttcc ttagcctcct ggtttgtgtc ttttttttct ttttttaaac 900
acagaatcac tctggcaatt gtctgcagct gccactggtg caaggcctta ccagccctag 960
cctctagcac ttctctaagt gccaaaaaca gtgtcattgt gtgtgttcct ttcttgatac 1020
ttagtcatgg gaggatatta caaaaaagaa atttaaattg tgttcatagt ctttcagagt 1080
agctcacttt agtcctgtaa ctttattggg tgatattttg tgttcagtgt aattgtcttc 1140
tctttgctga ttatgttacc atggtactcc taaagcatat gcctcacctg gttaaaaaag 1200
aacaaacatg tttttgtgaa agctactgaa gtgccttggg aaatgagaaa gttttaataa 1260
gtaaaatgat tttttaaata tcaaaaaaaa aaaaaaaaaa ctcga 1305

<210> 19
<211> 1060
<212> DNA
Homo sapiens

<400> 19
gaattcggca cgagaatcaa tctacaccct caagcagttt gtagtctgct ggaatgacag 60
acttaaaaat gcttataact aaaatatttt atgtgcagga ctagggtttt taagctaaaa 120
ggctgctttt taaattgtga aatataaagt acatgtagaa caatgcataa aacatgtcaa 180
cagttaaaca gatagttatg ggattatact ttgtgtatwt ttatgtttgc ttcttttatt 240
caacattctg tggttcatct gtgttgcttg tagcatcatc attactgtag catactttat 300
ttgttctact gttggtggac attactgttg cttccagttt ttggctatca ttaacaatga 360
tgctaagagt gttcttgatt atttgtcttg gtatgtttgt gcacgcacca ataatatata 420
tctaggaatg gaatcgttgg gtcatagaga atatacgtag cttttaagtt tactagataa 480
gtgatttttcc aatttaaaaa gacctttgaa acgtttttct acattggtgg tttttaaagt 540
tatctatttt ctcatggaat ttggtttttct catgagaata aggtaggaat ggttgtatgt 600
tgctaatatg tagttcaagt gccctttcta cctaatctgg attgccagga atatgcttga 660
aatgccaaat catgacttag tattttmctg tggtaattgg agtagtcttt gacacatcag 720
gaagtatggg aatatgggaa agatctttga gagtggaaac tataccacag ttttgtttag 780
tgctaggtag gaaaggtgaa aaaaaaagcg cgagagtata ttaagtatac aaaaagctta 840
gtggttttaa aatgttaagc tcacatttgg aagtgtaatt ctattttaat ctctttccta 900
atggaggaag aaagatgact gatgtggtag ggtaatcttg tttgaaaaat tgacaactct 960
ggcatacggc ccagatctct tttcagattt tgtgtgaaaa agaaaaatgg cagcctctta 1020
gtgctattca ttggtgtaaa aaaaaaaaaa aaaaactcga 1060

<210> 20
<211> 1170
<212> DNA
<213> Homo sapiens

<400> 20
ggttaacatt tgtggatgac tgaagattga tggaatgcta ctatgccaaa ccttaattgt 60
gatattattt tcataactga attattttag aaatgtatca attgactgct gctcagcagt 120
aactaaaatt cctcaagtat ttgattaaac agaataatgt caaaatttaa accttccctt 180
aaaactttat acataagaca tttatgattg ttcaattttt ataatctatt tgtggatttt 240
gttaaaagat ttcacatgaa gatttattag ttgccattta aaatttttat atgtttagtt 300
aaaagatttg acatgaaaat ttattagata ccatttaaaa attttatgtg ttatgtgttt 360
attctttgag aatgttacct tactgtttgt aatagtgcta catttttctg ctttcaggcc 420
tctgtatttt cacaaaacac caaaaacagc atttaattat attatcatga gtgtgtttct 480
ggacacaaac ttctgcagta gaatgaccta acatgtcgtt ttcattgcag tcattatagg 540
attgaaatac gttcaaaata acctctctag gaaagtcttc tgctagaatt tctcccctct 600
attcattata atattctttg tttttaaagc cagtcaaata taatagtctt aataagatca 660
gaaactctcc aggagagtga gtctaccctc acgtccttgt aggatgatct tgattatagt 720
cttattatag gactataact gtattctcaa catttctcca gaaaggacct tgtaaaaagg 780
tcttttgtac cacagtattg gtttttttccc ctctctcttc acttaaaaaa aaaaatagca 840
aggcagaaat agtgtattga aaagttgttc atctattatg aagtccttga gtggtgaaaa 900
atccgttgta catgagaaca tttctatgca tttaagccag aaacgaggta catggctgtg 960
tgctcttctg tcaaccaatg aaatgtgttt tcacatgtgt ggcagtgcaa gtaaataaca 1020
cattatttga ctgaatcagg catgatactg caccaaagtg ttggtacata ttcacggtag 1080
taaatcagta cccctgttaa aggatttatc ccattgcttc atattaataa aatggttaca 1140
atatatcaaa aaaaaaaaaa aaaaactcga 1170

<210> 21
<211> 2084
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (2075)

<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (2083)
<223> n equals a,t,g, or c

<400> 21
ggcacgagga gttgtgcaga tacctggctg agagctggct caccttccag attcacctgc 60
aggagctgct gcagtacaag aggcagaatc cagctcagtt ctgcgttcga gtctgctctg 120
gctgtgctgt gttggctgtg ttgggacact atgttccagg gattatgatt tcctacattg 180
tcttgttgag tatcctgctg tggcccctgg tggtttatca tgagctgatc cagaggatgt 240
acactcgcct ggagcccctg ctcatgcagc tggactacag catgaaggca gaagccaatg 300
ccctgcatca caaacacgac aagaggaagc gtcaggggaa gaatgcaccc ccaggaggtg 360
atgagccact ggcagagaca gagagtgaaa gcgaggcaga gctggctggc ttctccccag 420
tggtggatgt gaagaaaaca gcattggcct tggccattac agactcagag ctgtcagatg 480
aggaggcttc tatcttggag agtggtggct tctccgtatc ccgggccaca actccgcagc 540
tgactgatgt ctccgaggat ttggaccagc agagcctgcc aagtgaacca gaggagaccc 600
taagccggga cctaggggag ggagaggagg gagagctggc ccctcccgaa gacctactag 660
gccgtcctca agctctgtca aggcaagccc tggactcgga ggaagaggaa gaggatgtgg 720
cagctaagga aaccttgttg cggctctcat ccccccctcca ctttgtgaac acgcacttca 780
atggggcagg gtccccccaa gatggagtga aatgctcccc tggaggacca gtggagacac 840
tgagccccga gacagtgagt ggtggcctca ctgctctgcc cggcaccctg tcacctccac 900
tttgccttgt tggaagtgac ccagcccccc ccccttccat tctcccacct gttccccagg 960
actcacccca gcccctgcct gcccctgagg aagaagaggc actcaccact gaggactttg 1020
agttgctgga tcaggggggag ctggagcagc tgaatgcaga gctgggcttg gagccagaga 1080
caccgccaaa acccccctgat gctccacccc tggggcccga catccattct ctggtacagt 1140
cagaccaaga agctcaggcc gtggcagagc catgagccag ccgttgagga aggagctgca 1200
ggcacagtag ggcttcttgg ctaggagtgt tgctgtttcc tcctttgcct accactctgg 1260
ggtggggcag tgtgtgggga agctggctgt cggatggtag ctattccacc ctctgcctgc 1320
ctgcctgcct gctgtcctgg gcatggtgca gtacctgtgc ctaggattgg ttttaaattt 1380
gtaaataatt ttccatttgg gttagtggat gtgaacaggg ctagggaagt ccttcccaca 1440
gcctgcgctt gcctccctgc ctcatctcta ttctcattcc actatgcccc aagccctggt 1500
ggtctggccc tttctttttc ctcctatcct cagggacctg tgctgctctg ccctcatgtc 1560
ccacttggtt gtttagttga ggcactttat aatttttctc ttgtcttgtg ttcctttctg 1620
ctttatttcc ctgctgtgtc ctgtccttag cagctcaacc ccatcctttg ccagctcctc 1680
ctatcccgtg ggcactggcc aagctttagg gaggctcctg gtctgggaag taaagagtaa 1740
acctggggca gtgggtcagg ccagtagtta cactcttagg tcactgtagt ctgtgtaacc 1800
ttcactgcat ccttgcccca ttcagcccgg cctttcatga tgcaggagag cagggatccc 1860
gcagtacatg gcgccagcac tggagttggt gagcatgtgc tctctcttga gattaggagc 1920
ttccttactg ctcctctggg tgatccaagt gtagtgggac cccctactag ggtyaggaag 1980
tggacactaa catctgtgca ggtgttgact tgaaaaataa agtgttgatt ggctagaaaa 2040
aaaaaaaaaa aaaaaaaaaa actcgagggg gggcnccggt acnc 2084

<210> 22
<211> 643
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (115)
<223> n equals a,t,g, or c

<400> 22
gaattcggca cgagaaacta tctcaatcga tgatgtttcc acaaagaact tctcacaagc 60
agaaatggga ggccaagcct cac cgaccttttc agaagcactt gcaangcaca 120

caggacatgt tgccgtacag cctgcctttt cacatttcct gtacttcttc tctgagccac 180
catcttcayc ctcatctgtt gtctctgttg ctttcttttt cgcctaaggg agtcacagct 240
gatgttaaaa tttcactgat gatggcaaaa tgactaagga tgaaggttca ctactgaaat 300
cacagctgag ttctaaacat gaaggtcaaa aacwtcatgg cagtaggtta gggatgacaa 360
tacagcaatt tcctggtgac tgcattgtgc aagtaattta ctaacttgct agagatatag 420
aaatagcatt ttaacaacag atgtctaagc caagaactaa attcatatga gtctttctta 480
gaaaaaagtg acatcagctg ggtgtggtgg ctcatgcctg taatccccag cactttgggt 540
ggctgaggtg gaaggatcac ttaagctcag gagtccaaga ccagcctggg caacataccg 600
agacctcctc tctactaaaa aaaaaaaaaa aaaaaaact cga 643

<210> 23
<211> 647
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (69)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (614)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (632)
<223> n equals a,t,g, or c

<400> 23
nccaaagttc gaaattaccc ctcactaaag ggaaccaaaa gctggagctc caccgcgttg 60
gcggccgcnt ctagaactag tggatccccc gggctgcagg aattcggcac gagagctgcc 120
ttggctcggc ttggtctgcg gcctgtcaaa caggttcggg ttcagttctg tcccttcgag 180
aaaaacgtgg aatcgacgag gaccttcctg cagacggtga gcagtgagaa ggtccgctcc 240
actaatctca actgctcagt gattgcggac gtgaggcatg acggctccga gccctgcgtg 300
gacgtgctgt tcggagacgg gcatcgcctg attatgcgcg gcgctcatct caccgctctg 360
gaaatgctca ccgccttcgc ctcccacatc cgggccaggg acgcggcggg cagcggggac 420
aagccgggcg ctgatactgg tcgctgacag cgccaaagag accaacaaga tgattttagc 480
gtggactagg acacttaacc taagaagagt ttcacttaat cattcaaatc actatctgaa 540
gggtcacgga gcgcaaaata aagtttaaaa ccctgctacc aaaaaaaaaa aaaaaaaaaa 600
ctcgaggggg gggnccggta ccccaatttc gncctatagt ggagtcg 647

<210> 24
<211> 825
<212> DNA
<213> Homo sapiens

<400> 24
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gaccagcctg gccaacatgg tgaaacccgt ctctactaaa aatacaaaaa gtagtcaggt 660
gtggtggcgc atgcctgtag tcccagctac tcaggaggct gaggcacgtg aatcacttga 720
gctagggaga cggaggttgc agtgagctga gatcgtgcca ctgcattcca gcctgggtga 780
cagagtgaga ctctgtttaa aaaaaaaaaa aaaaaaaaaa ctcga 825

<210> 25
<211> 541
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (11)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (12)
<223> n equals a,t,g, or c

<400> 25
ggacccccgg nncaggaatc ccccccccc ccccccatct gtctctccag atcttaccca 60
tcttgtcctt ccacacgtcc ccgatgcctc tgaagatgcc attcatgttt ctctcccttc 120
cccgggacac attcctaatg ttggagttgg tgttaggtac tttcacttgc aatgggagtt 180
tctttattca caaagcctct tgagtgttgc tctcatacta ttttgtgtgt ccttccaggg 240
cagtgacctt gacagttatt tgtcttgttc tcccaagcgc gggtgctaag gacatagtct 300
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tggtggaaat tcagatccaa actgtatctc cagggcatga tggcgcctgt ctgtagtgca 420
gttacttgag aacttgggag ggtgagttgg gaggatttct tgaggttcca ggagttcgag 480
accaacttgg gcaacatagc aagatcctgt ctctataaaa aaaaaaaaaa ggatccctcg 540
a 541

<210> 26
<211> 852
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (719)
<223> n equals a,t,g, or c

<220>
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<222> (834)
<223> n equals a,t,g, or c

<220>

<221> SITE
<222> (840)
<223> n equals a,t,g, or c

<400> 26
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atccgaaagt ggtagttcca atgccaagga gcctaagacg cgcgcaggcg gtttcgcgag 180
cgcgttggag cggcactcgg agcttctaca gaagggttct ccaaaaaatg tggaatcctt 240
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ccggttgcgg ctattagatc ttgaacttac gtctaggttc ctgggagcaa caacagatac 480
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ttggtggggg gg 852

<210> 27
<211> 4598
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (948)
<223> n equals a,t,g, or c

<400> 27
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gggcaggaag tcaggcagca gggaaggaca cgggaacagc aggtggagaa ttcctacagt 180
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acctgatcat gaggaagacc aggtttccag tgtaaactac tcttgttccc accacctctg 660
gagcactcag ggagccccat acagtactta caatgtcttt aatggacttg attctgttta 720
atttttgtt ttatattagg cacactgtat taattttcca aaatgttata ccacactatg 780
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tcttttgttg caaaaaaaaa aaaaaaaaaa aaaaaaaa 4598

<210> 28
<211> 585
<212> DNA
<213> Homo sapiens

<400> 28
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tttgatcttg ctagaacatg ttcagggaag gtgttcagac aacaactagg actaatattc 180
cttcaagggt cattaaatgg ttgattaact gaaacatcaa gggattatag atcaggcatg 240
tgtaggcaat gacaactatg tcatgactgc tgtgtggcca acagtaattg aaggctgcca 300
tcaattataa gacacattcc atttcagaga tgttacagtg tggggtgggg gaaagtctgt 360
ctggaattag tagtaaggga cctgtcttat aataggcaga aaatgtgtgt aattgaatct 420
taagtatata acatctaaag aattataaga ttttagagcc aggaataaaa aaacacatgt 480
taccatccct tagaatctta gaaaatgtta ttggtgaaat aaactttagt gatgatcata 540
cagaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa ctcga 585

<210> 29
<211> 824
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (759)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (791)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (792)
<223> n equals a,t,g, or c

<400> 29
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tctgatctta tgattcaccc acctctacct cccgaagtgc tgagattatg ggcgtgagca 120
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aatatggatt gtatgtgtat ttatatgttt ttaatcattt tgatcaatgt ttgtagattt 300
caaggtacaa acttctcacc tttatatgtt tattcctaaa tatttcttac tttaagctct 360
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aaaaaaaaaa gggcggccgc tctaaaggat ccaagcttac gtacgcgtgc atgcgacgtc 660
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<210> 30
<211> 773
<212> DNA
<213> Homo sapiens

<220>
<221> SITE

<222> (2)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (773)
<223> n equals a,t,g, or c

<400> 30
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cctcctccty ctgctgggcg ctgtcctgaa tccccacgag gccctggctc agmctcttcc 120
caccacaggc acaccagggt cagaaggggg gacggtgaag aactakgaga cagctgtcca 180
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gtttgacctg ggcttcccca atcccttggc agagaggatc atctttgaga ctcaccagat 360
ccactttgcc aactgctccc tggtgcagcc caccttctct gacccccag aggatgtact 420
cctggccatg atcatagccc ccatctgcct catcccctc ctcatcactc ttgtagtatg 480
gaggagtaaa gacagtgagg cccaggccta gggggccacg agcttctcaa caaccatgtt 540
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tcatccccac cacagatccc tggattgctg ggaatggaag ccaggtgggg tcatggcaca 660
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<210> 31
<211> 969
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (36)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (123)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (347)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (525)
<223> n equals a,t,g, or c

<400> 31
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<210> 32
<211> 1355
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (111)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (113)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1332)
<223> n equals a,t,g, or c

<400> 32
ggaattngtg ancgattaca atttcaccac aggaaaccag ctatgaccat gattacgcaa 60
agctcgaaat taaccctcac taaagggaac maaagctgga ctccaccscg ntngcggccs 120
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<210> 33
<211> 536
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (20)
<223> n equals a,t,g, or c

<400> 33
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gatttgggtc aggaaacaga gccaaaccat atcaagagcc tctggtaacc actgttctac 180
tcaatacttc tatgaggtga acttctttgg attccacata tgatcaagat catgaggaag 240
gaggagcaag tcttctttgt catgctatta agaaaatacc cagagtcaca gcaccatgat 300
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ctgcaaataa agacaacttg agactggata atttaaaaaa aaaaaaaaaa aaaaaa 536

<210> 34
<211> 1123
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (78)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (79)
<223> n equals a,t,g, or c

<400> 34
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taaatattga gaagatacac tggggagata gcatataaaa atgatgctcc [illegible] 180
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aattaaaaag tacaagagtt tgctcatata aatcaagttg cccaggaaac [illegible]gg 300
gctatcattt gtctcataat ttagaaacgt gatctcttga gagagagac [illegible] 360

tgggcacttt cagattcctt aggaagtgcc cctttgatat ttggaatgtg gatatattta 420
taaaacaaat ggattgttat tccaaatcca catggattta taaccaagcc ccagaagaat 480
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tggaatttgt gagggacatt ttgtggatgc cttaaagatg accagtggtg ggttctgatg 660
ggaatatata cactcatctg gactaggcca atggaagcag tctctttcag ttcacctccg 720
tacagcacaa gttgttcctg ctcatgacct cattgaggaa aatgagaatt gtggtgctgg 780
tgactttcat gtgtcttggg aggttgaggt gttcaacatc gttaaggcac tcccaaaacg 840
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gttttcatgg tttgtttttt acactatatt tctcattagg ttctttaaac atcaggttta 960
atattgatat tatgaataat ttttaaacca aagtattcta taagtctgtg tgctttgttt 1020
tcctggatgg tttgaccaag gtaaacatca gtcttgtcct tctctcttaa taaagtcatc 1080
catttgttaa gaaaaaaaaa aaaaaaaaaa aaaaaaaact cga 1123

<210> 35
<211> 587
<212> DNA
<213> Homo sapiens

<400> 35
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ataaggagat tttagataat ggggaaaaat ccagaaaaaa aatttacaat aatcttgcta 180
ctgattataa catcatctct tgctgacatt tctttaaggg gttagtctag tatgtcaagc 240
atatgcagct gcttggagct cttgattttt agaaatgaat aatacaagag aaccaactaa 300
tgttccttag ctcttcaaac cagtctagta cctgcatgaa aacattggtt attttggtat 360
ccagttggag agcacagggc catgcagcag gatttctgaa aatcaaagct ctcttcctga 420
aatatatggc cacaaaggat gcatttctgg gatctgatgt ttcctggctt attcaaataa 480
taatgatggt gttaggaaac ttttacaact ataggcctct tcttttcttt atgctcaatg 540
cctcgtgccg aattcgatat caagcttatc gataccgtcg acctcga 587

<210> 36
<211> 842
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (823)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (826)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (831)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (832)
<223> n equ r c

<220>
<221> SITE
<222> (838)
<223> n equals a,t,g, or c

<400> 36
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agcatataca gatttccttg ggaaatctgt ggtattaaat tctttccatg aagattaaaa 120
tcattaaaat gtattttatt tacttaaaat atattttatt gactccagga gtaggcatga 180
atgagacaag atagaatgaa aaacaaaaac agctagccct ctgtcctgtc ttttgctgag 240
gtcctctgac tctctctgag atggaaaagg tgaagggtca agcagcctag ttcaggcaca 300
cgaggggact actaatatta catcagttaa aagtkgcaac atttccaagg agaattctac 360
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tkgtccacaa ccaaatgaat ggataattgt ccatgtcggt gttctaagtg ctactcttaa 480
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cacctaggaa ccctgacatt cttctgcttt cctaggagaa ggagagtcag agctaacaaa 600
ttaattttaa aaaggctctg aacaagaatt ttatcaaatt accactttga ttttgcctgc 660
taggatgtca taacctagaa tctcatccct taatatataa cagtttagtt taaccgaggc 720
atttttcagc ctatgagacc gaagtgacat ctaacaaact ggtcttatta gaatttgcct 780
gtatgggagg cctcgtgccg ctcgtgccga attcgatatc aanttnaagc nnacctanta 840
ct 842

<210> 37
<211> 953
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (952)
<223> n equals a,t,g, or c

<400> 37
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gatacaataa tttttagctt tttatttttа attattctgg ttgttaccta cataactctg 120
ggcaatatgg aaaagttatt gattttgtat attaatttca taatcagtta ccttgatgaa 180
ttctcttgtt tctagtagtt tttctttagg gttttaaagg gatacaatca taccatttgc 240
agttagtaac catttatctc ctcttatttc caacttcgta ctgttttctc ttgtctaatt 300
tgtttttaat tggtgggtac ttctagaaca aggttaaata aaagtggtgt tggtgggcgt 360
ccttatttct gatattaatg ggaatgagta taatgtataa atatataacc atgattttgg 420
ttttttcca agtttttatc agtaatgatt gctgagtttt atcaaaattt ttttggcatc 480
cattgagagg attatatatt actctttgac acattaatgt ggttaattaa agtaaccaac 540
ttattaacct tgaaatagtc ttagttaaat aamccctact tgtcaatgct atatcattat 600
tttaatattg tactgaacat tttacaaagg tgtttcacca taaggcatat tgatctgtaa 660
ttttttttt tctgttgaac ttgctattgt caggttttgg tgtattatgt tggttttgga 720
gaataaattt aaaagtttcc tttatgttat ctatacattg cctgaaaaga gtttaaatag 780
cattgaaaat gatctcttct ttgaagattt aaccaatttc acctgtaaat ctgtctgtgc 840
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atttttctat taaaaatgta aaatcaaatt ataaaaaaaa aaaaaaaaaa cnc 953

<210> 38
<211> 2211
<212> DNA
<213> Homo sapiens

<220>

<221> SITE
<222> (2181)
<223> n equals a,t,g, or c

<400> 38
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gatggggagc gtcctggggc tgtgctccat ggcgagctgg ataccatgtt tgtgtggaag 120
tgccccgtgt ttgctatgcc gatgctgtcc tagtggaaac aactccactg taactagatt 180
gatctatgca ctttttcttgc ttgttggagt atgtgtagct tgtgtaatgt tgataccagg 240
aatggaagaa caactgaata agattcctgg attttgtgag aatgagaaag gtgttgtccc 300
ttgtaacatt ttggttggct ataaagctgt atatcgtttg tgctttggtt tggctatgtt 360
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cttttgtttc atcctcatac aactagtctt acttattgat tttgcacatt catggaatga 600
atcgtgggtt gaaaaaatgg aagaagggaa ctcgagatgt tggtatgcag ccttgttatc 660
agctacagct ctgaattatc tgctgtcttt agttgctatc gtcctgttct ttgtctacta 720
cactcatcca gccagttgtt cagaaaacaa ggcgttcatc agtgtcaaca tgctcctctg 780
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gtatgttttt gcttcccatg taacttctcc agtgttctgg catgaattag attttactgc 1560
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gaaggattta gacaaggttt tgaaaaggat aatcatgggt tagaaggaag tgtttgaaag 2160
tcactttgaa agttagtttt ngggcccaca cggttggctc acccctgtaa t 2211

<210> 39
<211> 682
<212> DNA
<213> Homo sapiens

<400> 39
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cactggctcg gaaggggtg gaggttgctg gagggtggag agaaggagct gccaacctgg 120
tcactgttgt tgctgtatcc aggttgcctc cagtcctgct ccaccacacc atggaccact 180
ccatcccaga tgcctgaagc cactggaggg cagggcaatc agggcaggct tcccgccctc 240
ctgcagcaaa gggcaaccac cctcggatga tggg[illegible] gcttaaggtg 300
ggggctgcca tgaggggggc gtgtccagga gggt[illegible] atacacacag 360
gcctccttgg agcctcagac tccaagctag gctg[illegible] caggcagc 420
cgattctctt gtgctgattt aaatgctgga cac[illegible] gctgctta 480

aagtcgcaac tgggcccctt tcaagaaatt ttgctctacc aggaaaacag ttacacattt 540
taagagaaca gagctacgtt ctttgtgaga gctttttcct tgscttgact tgctctttgt 600
cacagactgc ataagttgtc agccttgact atcttttgaa taaagatttg attttaaaca 660
aaaaaaaaaa aaaaaaactc ga 682

<210> 40
<211> 685
<212> DNA
<213> Homo sapiens

<400> 40
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tgctgcttct gggtcctgct gtcccccagg agaaccaaga tggtcgttac tctctgacct 120
atatctacac tgggctgtcc aagcatgttg aagacgtccc cgcgtttcag gcccttggct 180
cactcaatga cctccagttc tttagataca acagtaaaga caggaagtct cagcccatgg 240
gactctggag acaggtggaa ggaatggagg attggaagca ggacagccaa cttcagaagg 300
ccagggagga catctttatg gagaccctga aagacatygt ggagtattac aacgacagta 360
acgggtctca cgtattgcag ggaaggtttg gttgtgagat cgagaataac agaagcagcg 420
gagcattctg gaaatattac tatgatggaa aggactacat tgaattcaac aaagaaatcc 480
cagcctgggt ccccttcgac ccagcagccc agataaccaa gcagaagtgg gatgcctgtc 540
ttgagtagac ttggacccaa aaaatcatct caccttgagc ccacccccac cccattgtct 600
aatctgtaga agctaataaa taatcatccc tccttgccta gcaaaaaaaa aaaaaaaaaa 660
aaaaaaaaaa aaaaaaaaaa aaaaa 685

<210> 41
<211> 550
<212> DNA
<213> Homo sapiens

<400> 41
gaattcggca cgagggttca gattagaatg ggtctgttta atcagtgtga ttacagtgat 60
ccaagtttgc agttagtttt ttttttaatg gctctattcc acattttgtt ttcattaact 120
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ctctaccact ttttttcata attggttttc attctagaat ggaaaagaaa atggtgtagt 240
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gtggtgagat ttccatgaaa taatctaggg gaaagacttc atactgttct tcattcttgt 420
gctttactta tcctcaattt tgaaaaatgt ttttaaaaat aaattttatt ggctgggtgc 480
aggctcattg cattgcagcc tttgtgacaa gagcgagacc ctttctcaaa aaaaaaaaaa 540
aaaaacacga 550

<210> 42
<211> 602
<212> DNA
<213> Homo sapiens

<400> 42
tggatctcca ccgcggtggc ggccgctcta gaactagtgg atcccccggg ctgcaggaat 60
tcggcacgag attgtatcca ggaagtaact aacctgcttt tgattttaca ggctcatagg 120
tggaagggac ttgccttgtc tcagatgaga ctttagactg tggacttttg agttaatgct 180
gaaatgagtt aagactttgg gggactgtta gaaaggcatg attggttttg aaatgcgaga 240
tcatgagatt tgggag[illegible]gggcaga atgatatggt ttggctgtgt ccccatccga 300
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gggcaagtct [illegible]ttgtga tagtgaataa gtctcatgag atctgatggt 420
tttaaaaaga [illegible]agtt ctctctcttt gcctgctgcc atccatgtaa 480

gatgtgactt gctcctcctt gccatctgcc atgatgtgag gcttccccag ccacgtggaa 540
ctgtaagtcc aattaaacct cttttctttg taaattaaaa aaaaaaaaaa aaaaaaactc 600
ga 602

<210> 43
<211> 1627
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (618)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (627)
<223> n equals a,t,g, or c

<400> 43
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ggtggaggtg gtgtccccac tgagctcttg gaagagagtg gttgaaggcc tttcactgtt 120
gggacttggg agtatctccg tattctggag cagtatttca tggaaactcc attaaataaa 180
tatacctctt tcatttccta attgactatg ctgaattggt gtttatgata actgrtgcac 240
tcactgctat tgccctgtat tttgcaatcc aggacttcaa taaagttgtg tttaaaaagc 300
agaaactcct sctagaactg gaccagtatg ccccagatgt ggccgaactc atccggaccc 360
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cgattttgtc ttgtgttgcc aagtctacct gtgccatcaa caacaccctc attgctttct 480
tcattttgac tacgataaaa ggcagtgctt tcctcagtgc tatttttctt gccttagcga 540
cataccagtc tctgtaccca ctcaccttgt ttgtcccagg actcctctat ctcctccagc 600
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tctgcacacc aaggagcccc ctcccagaca ggaaggagaa gaggcaggtg agcagggctt 1560
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ggcggcc 1627

<210> 44
<211> 1457
<212> DNA
<213> Homo sapiens

<220>
<221> SITE

<222> (879)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1397)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1425)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1448)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1455)
<223> n equals a,t,g, or c

<400> 44
ctgatcccct gctcatcaat gacttcaagg atgtgacgca cacatgcccc agctgcaaag 60
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gtcagtctgg ccccctgtgc tttgctccct gygctcagtg gtcactttcc cgctcccact 180
tggggctggg agccgtgcca ccatccccta gaagtcctgt cctcttcacc ctgccctacc 240
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ggttcagtcc agactctttc cccctgggac caacagcagc cagagcagtt agccagttag 480
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caatcgccct atatgantcg tattacaatt catggccgtc gtttnacaaa gtcgtgactg 1440
gggaaaanct ggcgnta 1457

<210> 45
<211> 888
<212> DNA
<213> Homo sapiens

<400> 45
gaattcggca cgagacagag tgtgggatag atcatatatg catcca 60

atataaccat cttgaatagt aattgctcac ctgcattttg taacaagagg ggcatctgca 120
acaataaaca tcactgccat tgcaattatc tgtgggaccc tcccaactgc ctgataaaag 180
gctatggagg tagtgttgac agtggcccac cccctaagag aaagaagaaa aagaagttct 240
gttatctgtg tatattgttg cttattgttt tgtttatttt attatgttgt ctttatcgac 300
tttgtaaaaa aagtaaacca wtaaaaaagc agcaagrtgt tcaaactcca tctgcaaaag 360
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cctcccagag ccaacctcgg gtgacaccct cccagagtca acctcatgtg acaccttacc 780
ggagtaaaag tggtaaacaa aagcaatcag taccaattcc aaaaactgta tccagaaaag 840
gtacattaaa aaaataattc ctaaaaaaaa aaaaaaaaaa aaactcga 888

<210> 46
<211> 752
<212> DNA
<213> Homo sapiens

<400> 46
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ccactcatct ggccaccgtt gccctgacct gccaggagcc tggagaagat gaaggcatcc 120
gtggttctct ccctccttgg ctacctggtg gttccaagtg gtgcttacat cttggggcgt 180
tgcacagtgg ctaagaaact ccacgatgga ggcctggatt attttgaggg ctatagcctt 240
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ggcgaccatg gcaggaaccg ctgccatatg tcatgttccg ctttactgaa tcctaattta 420
gagaagacaa ttaaatgtgc caagaccatt gtaaaaggaa aagaagggat gggagcatgg 480
cccacctggt cccggtactg ccagtactcc gataccctgg cacggtggct ggatggttgc 540
aagctgtagc ckcctgcatg gcccctgcag cactcaccag ttgcatcttg tgaatgaagg 600
tgcttttctg cttgctgctt cagtcaatcc ttttgatgat ctcaccactt taagagttcc 660
agatggaaaa agacaaaagt ttgcttcatc cggggatgca ggatgcagaa taaaccaaac 720
tagttactca aaaaaaaaaa aaaaaaactc ga 752

<210> 47
<211> 1788
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1490)
<223> n equals a,t,g, or c

<400> 47
gtatgttcct [illegible] ctctaaattg tactcaattt catggtaatt acatgaagaa 60
gttacctg[illegible] [illegible]acttacatg gtaattcact gggtaattgt gggtcattta 120
tttcctga[illegible] [illegible]ttagctg gttgaatgtt gcacagtatt tgagaattac 180
ggtttgaa[illegible] [illegible]aatc attgcaatgt atattctaaa taaagtcatc 240
taacta[illegible] taa cccttctttt cttaaaattc cacattcatc 300

cacaatctca tccctttgta gaaattcttg cctgaattct caccaagttt tgaattccta 360
aggtagcccc gatctaggat gtgaaggctg cccagaaaaa gtttatggct ggaggagtat 420
catacagtgt ctacatatga tagtacttac agattaggtc ttkggatgct ttaacacaaa 480
agatttttgt tatccttatt agtcaaataa cgctattctt ttgtggttct agaccctggc 540
ttctatctcc ctgtgatttg ttttaatgct gaaatgactt ggctatccaa agcttctagt 600
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ctagcttacg tgaatgatgt tgccctcatt tgttttgggt gaggactcat tactgcagta 720
tattgatctc ttcaccaaat gctttttcty tttctgaata aatgctgtat tagaggttct 780
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aatcattckg gggcaaakgc tctattatcc ttatttatga caagagaata atgaaattca 1020
taagaaatta ataacattca gatattgcta taaatgtact tgagtcattt tcatttgggg 1080
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tgccatgaaa tgattgcttt tctttttctt ttttttttcct taaataaaaa taatgcagcc 1440
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gtaatcccag acctttggga ggctgacacg ggaagattgc ttgagcccag gaatttcaga 1560
ccagcctggg caacacagga agactccatc tctacttaaa atatttttgt tttttagcca 1620
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tgaacccagg agtttggggt gcagtgagct atgattgcga cactgcactc cagcctgggc 1740
aacagagcaa gaccctgtct caaaaaaaaa aaaaaaaaaa aaactcga 1788

<210> 48
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (393)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (401)
<223> n equals a,t,g, or c

<400> 48
gaattcggca cgaggagatg cacatggccc tgaacaacca ggccaccggg ctcctgaacc 60
tcaagaagga catccggggc gtgctggacc agatggagga catccagctg gagattctca 120
gggagcgggc ccagtgccgc actcgagcca ggaaggagaa gcagatggca agcatgtcga 180
aagggaggcc aaagctggga agytccaagg gcctggcagg ccagctctgg ctgctgaccc 240
tgaggctgct gctgggcgcc ctgctggtct ggaccgytgc ctacgtgtac gtggtgaacc 300
ccacaccttt cgaggggctg gtgccamccc tgctgagccg tgccaccgty tggaagctcc 360
gggccctgct ggaccccttc ctgcgcctca aantggacgg nttcctgccc ttctaggcca 420
raggcccagc ggccccagca aggaggccag gcgaccagca ctgccccgga tgcccagtgg 480
ccgtgccagc cccctgcaca tggcaccact gtgcaccatc cttgccagaa gctgcagaga 540
agggtggagg tggggtctgt cctgagggct gggcctgtgg ctggacatag agtcatgaca 600
taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaactcga 660

<210> 49
<211> 1321

<212> DNA
<213> Homo sapiens

<400> 49
ccggatcacc aggtcaggag atcgagacca tcctagctaa cacagtgaaa tcctgtctct 60
actaaaaata caaaacttat ccaggcatgg tggtgcatgc ctgtaatccc agctactcag 120
gaggctgagg caggagaata gcttgaacct gggaggtgga gattgcaatg agatgacatc 180
gccccactgc actccagcct ggcgacagag caagactcca tctcaaaaaa aagaaaaagt 240
catttggaag agatatgtgt agtgttgttc tgttaaaaga ctgtccactg ttttcttttt 300
cagtaattaa tggtcacaca ctgtgtttac ggctgttgct agaaattgca gacaacccgg 360
aggcggtcga tgtgaaagat gccaaaggac aaacaccact gatgcttgca gtagcatatg 420
gacatattga cgctgtttca ttgttacttg aaaaggaagc caacgtagac actgttgaca 480
tcctaggatg cacagcttta cacagagggg tatgtacatc tttctcagct ctagtcaagc 540
aatttttta atgagcttgt tttctttttt agcaaacaat tacaaagggc ctactttgat 600
tggattttta gcaaaaaatg tttagcaaaa attgtttcct aatacaacca attaacctta 660
ttcagtccaa aagaaattac aaaatccttg gcaaaggcaa aataatggaa ggttttgctc 720
ttaagatttc atgttagatt gtgataatag atgcatgaac acctactgct ggtgaaattg 780
gttctgcttt ctgactacaa aatacaagta tatcatagaa aatttgcaga atatttttt 840
ttaaagccca gagaagaaaa tcacaatcac cagtaatcat acctcctgga gataaccact 900
atttgatgta tattatctcc aatctttttt ctatatatag atttgtttta gattttaaaa 960
agagaatact gaagatatca tttggattct gctttttttct cttagtatat caaggatctt 1020
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acaaataatg ccaaaatatg tatcctgtgg gcaattattt gcacacatct gttgaagtgt 1200
ttggtttttt ttttttaat ctcactctta tcacccaggt tgcagtgagc cgagatcaca 1260
ccactgcatt ccagcctggg tgacacagcg agactccatc tcaaaaaaaa aaaaaaaaaa 1320
a 1321

<210> 50
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (10)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (14)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (27)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (68)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (533)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (539)
<223> n equals a,t,g, or c

<400> 50
ctcgaaattn accntcacta aagggancaa aagctggagc tccaccgcgg tggcggccgc 60
tctagaanta gtggatcccc cgggctgcag gaattcggca cgagcggaat ttgcggcttt 120
ggcagattga aatcatggca ggtccagaaa gtgatgcgca ataccagttc actggtatta 180
aaaaatattt caactcttat actctcacag gtagaatgaa ctgtgtactg gccacatatg 240
gaagcattgc attgattgtc ttatatttca agttaaggtc caaaaaaact ccagctgtga 300
aagcaacata aatggatttt aaactgtcta cggttcttaa cctcatctgt taagttccca 360
tgcctggaga agctaatgcc aactcatcat gtgataattc aatttgtaca ataaattatg 420
aacctggaaa aaaaaaaaaa aaaaaaactc gagggggggc ccsgtacccm attsgccctt 480
gkgrgkcgtt twccattcat ggcctsgttt tacaacgtcg tgactgggga aancctggng 540
ttacccaa 548

<210> 51
<211> 658
<212> DNA
<213> Homo sapiens

<400> 51
ggtcgaccca cgcgtccgtt ttctagtcta tgcataaact agaagaatgt gagaaaagac 60
tattttcagt tgctcatgtt tacctggatg aactagttta atttttgtct tttaaaacag 120
acatatttat tttaaaatta aaatagcttg aaattttaaa atacacccca aagcaagatg 180
atcgtttaag ttaagttaaa caatacaatg aatggtcttt tatttttggt gatgattgcc 240
aaaaacctct tgccttcagg aaataagcaa taaacctgat gaattgggca tagttgaggg 300
ggaaaataaa aatcaatggc ttctatttaa aaaacacagt atgtaatatc taaaaaagaa 360
aggcattgtt tctgaattgg ggtgaatgta ccaaacatat accaaaagga aggcattttg 420
ttagaaaatt tgattaatta ttagaatctt cctgactgga gatgtaaatt atcttgtttt 480
aaatctaact cactctaatt tggttttaat gttgactgta atccaggctg tttctgggga 540
caacagaaca caatatacct ctttattcaa accacacaat cttggccagc tattccctac 600
tccagcctga atgacagaaa gagaccttgt ctcgaaaaaa aaaaaaaaaa gggcggcc 658

<210> 52
<211> 622
<212> DNA
<213> Homo sapiens

<400> 52
ggtcgaccca cgcgtccgtt ctcatcatgt tatgggtgaa aacaaggaga gaagagctgc 60
ggcccttcgg ggaaccgaga cctggaagct ccctgaggca gggctgtgac tccctctttg 120
gacctcttaa gttcctggag tctcaagctt ccagccgcca ccatgtttcc tggtggcagc 180
tgtggaagct gcttctggtg tgcctggtcc agctgcagcc ttgcagagag ccggcaccca 240
tgcagacacc ttgtgctggc tgccccgctg cagcagctgg ggtgcctcac tgtgtgcagt 300
ggctggaccc catgctcact tgctcacaca cccctcactg ctccacacct ggcttgccgt 360
tggcagtgat gggatccagg ctggtagcgt gagctgagca cagcctgctc aagccaaatg 420
gatggaacaa acccagtggg ccagagcctc actcaggcaa aggtgccacc agccacagag 480
gcttctggsc agaaaagcaa cacctgg atcctgcaac agtagtttta caaagtgttt 540
attttgtcat ataaaaatct ggttt atttgcaaaa ataaaagtaa ggatgaaaaa 600
aaaaaaaaaa aaaagggcgg c 622

<210> 53

<211> 723
<212> DNA
<213> Homo sapiens

<400> 53
gggcgaccca cgcgtccgct cagcctttgt tgagagtgct gtgccccaaa tctggttggc 60
ttattctagg cattcgagtc tcttcccaaa taccaccttc tcaagtgcag cttttcctta 120
ctacttaatt ttatagtccc ccatcaatgt acgatgttac cctcttttcc ttcattgaga 180
gtgtttgtaa ttttttttg tctgcttgtt tattgtcttt ttgccccata agtccaaggt 240
ttacatgaac agggaacttg tctgttttgt ttattactgt atcccctatg ctggcacata 300
ctatgtaata agtgtttgtt gagtgcatga gtgaataacc attctaaaaa actctgatgt 360
ttaaagccct ttgctttata taagaatttt acttggaacc ctggtatttt cgtttgtatt 420
tgtttgttaa taaatgtcaa gagttcagta gtaagatagg tttcagaaat gctaagttaa 480
acagaataaa gaaagaatat gtattacagg tcctggcaga gccttgaata tgctaacatt 540
tgacagtggg agtctttgag aattatcaca tgaagctgct gtacattaca acacattcta 600
ggaaatgctg tcttagacaa aaacctgtca tattagaatt ggggtaaggg gcacgatact 660
gaccgtgagg cagcagattc ctatggacta cattaaaaaa aaaaaaaaaa aaaaagggcg 720
gcc 723

<210> 54
<211> 908
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (361)
<223> n equals a,t,g, or c

<400> 54
gaattcggca gaggggaggc ctgccctgcc cttcctcctg cagagagcca ggttcacagc 60
agggcgkcct gcaggacatt agcatgccta gtagatacac agtgtcgttg gggcgtgggc 120
attttgwttt ctgttccttc ttttttcccta tttaactatc atgtttgggg acctttgcct 180
ctcaattttt aagagattaa aaaaaaatga grgcggcctt tattatacac tacatgtgtt 240
ttctcccagt ttgtcagttg tcttttgcct ttttggtaat tttgccaggt acttatgtca 300
acttgcatta agatgtcccc ttattaataa aagtaatttg ctctcattgt atgcaattaa 360
nagaatacta aaatttctaa tgatcctacc acttaaagct gtataaacgc tgctaacata 420
ccaggtatcc cattccaggc ttgcttgtat gtgtatatat attaatattt atctgtagct 480
gtatgtctgk gacactctaa attattaaaa atttgtccca gtggcttaca aatttttttt 540
tgtagtagca gcagctttta aaaaatacaa atcttagcat agttaacaga aaaaaagagt 600
tgctccggtt aaggtagatt ctaatcccca ccagggcccc tgagacatgt ccttaaattg 660
ctacaaaatg tacaacaaac cactagtaaa gtttattcta tttgataact ctgtttgctt 720
ttaaaaactt catgtatagt gattattttc ctgttattct gtattcttca cctgcttcat 780
atttagtgac tgccaagtat tctattgtat gtttatgaca caagtaattt aactattttc 840
ttatcattga acatttacat ttgtatatac ttttactgtt ttgccaaaaa aaaaaaaaaa 900
aaactcga 908

<210> 55
<211> 822
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (361)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (817)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (822)
<223> n equals a,t,g, or c

<400> 55
tcgatccacg cgtccgcgga cgcgtggrgt tgaaaattca tagtaagatt gatatctata 60
aaatagatat aaatttttaa gagaaagaat ttagtattat caaagggata aagaaaaaaa 120
tactatttaa gatgtgaaaa ttacagtcca aaatactgtt ctttccaggc tatgtataaa 180
atacatagtg aaaattgttt agtgatatta catttattta tccagaaaac tgtgatttca 240
ggagaaccta acatgctggt gaatattttc aacttttttcc ctcactaatt ggtactttta 300
aaaacataac ataaattttt tgaagtcttt aataaatamc ccataattga agtgtataat 360
ataaaaaatt ttaaaaatct aagcagctta ttgtttctct gaaagtgtgt gtagttttac 420
tttcctaagg aattaccaag aatatccttt aaaatttaaa aggatggcaa gttgcatcag 480
aaagctttat tttgagatgt aaaaagattc ccaaacgtgg ttacattagc cattcatgta 540
tgtcagaagt gcagaattgg ggcacttaat ggtcaccttg taacagtttt gtgtaactcc 600
cagtgatgct gtacacatat ttgaagggtc tttctcaaag aaatattaag catgttttgt 660
tgctcagtgt ttttgtgaat tgcttggttg taattaaatt ctgagcctga tattgatatg 720
gttttaagaa gcagttgtac caagtgaaat tattttggag attataataa atatatacat 780
tcaaaaaaaa aaaaaaaaaa aaaaaaaaaa aanaagnaaa gn 822

<210> 56
<211> 1951
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (28)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1636)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1947)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1951)
<223> n equals a,t,g, or c

<400> 56
ggccctgggc tcgcggcggt gccgsggngg atggcgggag ccggagctgg agccggagct
cgcggcggac ggcggcgggg gtcgaggctc gagctcgcga tccaccgccc gcgcaccgcg
cacatcctcg ccaccctcgg cctgcggctc agccctcggc ccgcagatgg atggcgggct
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cgcgggcgtg acggcgctca gcatcccctg ctctacgtga agctgctcat ccaggtgggt 300
catgagccga tgcccccccac ccttgggacc aatgtgctgg ggaggaaggt cctctatctg 360
ccgagcttct tcacctacgc caagtacatc gtgcaagtgg atggtaagat agggctgttc 420
cgaggcctga gtccccggct gatgtccaac gccctctcta ctgtgactcg gggtagcatg 480
aagaaggttt tccctccaga tgagattgag caggtttcca acaaggatga tatgaagact 540
tccctgaaga aagttgtgaa ggagacctcc tacgagatga tgatgcagtg tgtgtcccgc 600
atgttggccc acccccctgca tgtcatctca atgcgctgca tggtccagtt tgtgggacgg 660
gaggccaagt acagtggtgt gctgagctcc attgggaaga ttttcaaaga ggaagggctg 720
ctgggattct tcgttggatt aatccctcac ctcctgggcg atgtggtttt cttgtggggc 780
tgtaacctgc tggcccactt catcaatgcc tacctggtgg atgacagcgt gagtgacacc 840
ccaggggggc tgggaaacga ccagaatcca ggttcccagt tcagccaggc cctggccatc 900
cggagctata ccaagttcgt gatggggatt gcagtgagca tgctgaccta ccccttcctg 960
ctagttggcg acctcatggc tgtgaacaac tgcgggctgc aagctgggct ccccccttac 1020
tccccagtgt tcaaatcctg gattcactgc tggaagtacc tgagtgtgca gggccagctc 1080
ttccgaggct ccagcctgct tttccgccgg gtgtcatcag gatcatgctt tgccctggag 1140
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ccttgggaca cctgcaagac gactccaacc caacaacaac cagatgtgct ccagcccagc 1260
cgggcttcag ttccatattt gccatgtgtc tgtccagatg tggggttgag cgggggtggg 1320
gctgcaccca gtggattggg tcacccggca gacctaggga aggtgaggcg aggtggggag 1380
ttggcagaat ccccatacct cgcagatttg ctgagtctgt cttgtgcaga gggccagaga 1440
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ctacccctcc agtcagccca gcgcccatcc tgcagctcag ctgggagcat cattctcctg 1560
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ggaggcaaat ggccangctc tgcctgtgtt tttctcaaca ctacttttct gatatgaggg 1680
cagcacctgc ctctgaatgg gaaatcatgc aactactcag aatgtgtcct cctcatctaa 1740
tgctcatctg tttaatggtg atgcctcgcg tacaggatct ggttacctgt gcagttgtga 1800
atacccagag gttgggcaga tcagtgtctc tagtcctacc cagttttaaa gttcatggta 1860
agatttgacc tcatctcccg caaataaatg tattggtgat ttggaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa gggggggnccc n 1951

<210> 57
<211> 663
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (64)
<223> n equals a,t,g, or c

<400> 57
ccaatcggct aattcaactc acatagtagg gaaacgtggt acnccctgca ggtacccggt 60
ccgnaattcc cgggtcgacc cacgcgtccg gctattgtaa tcttttctac ctatacttct 120
tcattggctc agaatgaagc aaggcatgtg ctgctttctt atatgtcatt tatgccataa 180
atcccattgt tagaaggtaa tgcttctaac ggattccatt catgcttttg agataaatgg 240
cattgacttt catattgatc acatggaaag ctgttacctg attcctttcc tgagatcact 300
tccagcctaa tgtgcatttg gctggaatat ggttgtctca gaataacatc atgcactcgg 360
gcttttatac ttctgccttt aggggactgt ggcagcatgc catgggtcaa gaagtacttc 420
tccttcatct tcctttgatg tcggtaactc atcctt[illegible]ctgcgtga gttgttaatg 480
cttttgtgtc ctccagttca catgctgatt gctaac[illegible]atgaaat gagtgaaccc 540
aaagctgctg aaacattctg cgtttatgca tcttt[illegible]tcta[illegible]aggaagatgg 600
tttcattgtc ttgtctagag aataaagtct [illegible]aaaaaggcg 660

gcc 663

<210> 58
<211> 778
<212> DNA
<213> Homo sapiens

<400> 58
ggcagagtca gctctgtgct gagcctcctg gcctggcccc caccggtgca tccgcccagt 60
gcgtccacct gccctggcta gcatgctgct gggccacacc ccaagatcag gggccctggg 120
gacggcaagt gaataaagca catttccacc caattttgtc atccgagaga gagcacaaac 180
tgcaggccct tgttgcagct gaaggaagac cctacagaga atggaattga gagtggagac 240
aggacacttc acaggacact tgagcacagt caagatttta ttcacacttt tggttcctgt 300
gttttatatc gaagacttag ctatgaattg ctatctaaat ctcagagctt agaagccaac 360
ccagtgacta gaccttccag tgaagaaagt gatctcaaga ggtccaggga cttaacagcc 420
aagccacacc acccgcacag gttcttctgt gacaccgaga gatctaaccc aaggcctggg 480
ttatgtctta gtcgagacat catcatctga gaagcaccac atcctttcag acacatcctc 540
ggacacacat gcggtccttg gtgcccccag gttcaatcct gcgttagctc ttttgatgag 600
aaggaaataa accaaaccag ccacttgcac tatggcttcc aagccaatgt tattgactca 660
ataagtgctt agcaattggc ttcctctttt gtcttcctat tttcagctcc atttaaacca 720
ggagttattt ataaagacct cttcctctca aaaaaaaaaa aaaaaaaaaa aaactcga 778

<210> 59
<211> 982
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (360)
<223> n equals a,t,g, or c

<400> 59
gaattcggca cgagcatatg tccaagtgtt accttgtcta gcccccagga acacagtccc 60
caggaccatg ttttttgggg cacccacagc aggggcagtg caggtctggt tgctcctgct 120
ctcacctgca gcatctcccg tagaggaatt gtcagttctg gttccctgtg ggcagtaaag 180
gtttccttgt aggtcactgg ggcattggcc agaaaaaggt tgtgaaaatc acatgctaat 240
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ccrggrgaat tgcttgagcc caggaggcag atgttgcagt gagccgagat cactgccact 600
gtactccagc ctgggtgaca gaatgagact ccatctaaaa aaatttttaa atttaaaaag 660
ttgacacact tttacaagct gcatcccatc tcagataagg aggtgatgta actgagttct 720
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tacataaaga ttctcctatg gttgggattt taaaaattca tagactactc aggccaggtg 840
cggtgcctca agcctgtaat ctcaacacat tggaaggcca aggagggtgg attgtctgag 900
cccagaagtt caagaccagc ctgggcaaca tggcaaaatc ctgtctctac aaaaaataca 960
aaaaaaaaaa aaaaaaactc ga 982

<210> 60
<211> 406
<212> DNA
<213> Homo

<400> 60
tcacacaacg ggtgatctca caaaactggt aagtttctta tgctcatgag ccctcccttt 60
ttttttttaa tttggtgcct gcaactttct taacaatgat tctacttcct gggctatcac 120
attataatgc tcttggcctc ttttttgctg ctgttttgct attcttaaac ttaggccaag 180
taccaatgtt ggctgttaga agggattctg ttcattcaac atgcaacttt agggaatgga 240
agtaagttca tttttaagtt gtgttgtcag taggtgcggt gtctagggta gtgaatcctg 300
taagttcaaa tttatgatta ggtgacgagt tgacattgag attgtccttt tccctgatca 360
aaaaatgaat aaagcctttt taaacaaaaa aaaaaaaaaa aaaaaa 406

<210> 61
<211> 813
<212> DNA
<213> Homo sapiens

<400> 61
gaattcggca cgagtctcag gtatgtttaa acccaatgtt tctttgttaa ttttctctct 60
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ggggaaaaat gaaggaatat gcctgctgtt tcctaatgag tagctgaaag tcttcaacct 180
atgaagcctc ctggatcatc tgccaattgt tcaacacaac tcccacccct gccttcatcc 240
tctttccctg attcacaccc tcatggcctc ttttcattac agtcaaggtc catcccagct 300
ttgacctcat gaatccatta tgccctcctc tgttactgct agacctgcag acccagtgtc 360
cacaaagatg ctcctatatt ctttattcct gcttctctgg aatggtttta atgcccccta 420
aagcaccagc wtgtgaatcg acctttgtgt tcatatcatg gagtcctctt agctccttgg 480
tgcctccaag gccaagcttc catcacctgc caagacacag cgagctggac caatatttgt 540
gtggcaggtt gggtgtgaca tgaatgtcaa agccaccctg aattgaggga ttctgctccc 600
ctttgttgaa cttcctttgg gtggtaagcc agacattgtc attcagcaaa catggtttca 660
ataaatatct agatgcaatc aagagaaaca tgaaaatgac atggcctcag tcctccaaga 720
gttcaaatct aacagaaggg acaaaaagtg tcttagccta agatgattaa aaaaaaaaaa 780
aaaaaactcg agggggggcc cgtaccctct cgc 813

<210> 62
<211> 846
<212> DNA
<213> Homo sapiens

<400> 62
gaattcggca cgagtctttc tgtttttaat gctttattac atatgcctag ttttgcttaa 60
gcttgtctaa attttatgac ggaactataa aaaatgtatt tcacttttac gtgacatgtt 120
attggtgaat cttgtgtttg tatgtttttt tctttttgaa aggagagtgc atttaaaatg 180
ctgaattgaa caggacatct tgagagaatg ttttaatttg agctcatgta tctgctgatc 240
gattctaagt gcaggatatt ttctgtttgt catagatatt tgaatggtgg tacttccata 300
agcatggcac atcttttatt gagcaagtat ctgtaagcca tttgcaacca ctgatgggag 360
gaacagagag cagcatttca gaaccaggtt ctccttcgag gaacagagaa aatgaaacca 420
gcagacagaa tttgtcaggt gactactttt ctaatgtgtt ttcagagctg tgtatttaag 480
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ttgtgtttcc cccaaaattc taatcaccaa tgtgatgtta cgaggtaggg tctttgggag 600
gtgatcaggt catgagggca gtgccctcag ggatgtgatg aatgcccttа tgagagaccc 660
cagagagctg cttgccactt ctaccgtggg aggacaccac gagaaggcgc cgtctgtgaa 720
ccagaaagca gaccctcacc agacaccaaa tttgttggta ccttggtcat agacttccca 780
gcctccagaa ctgttaaaaa taaatttata ctgtttataa tctaaaaaaa aaaaaaaaaa 840
actcga 846

<210> 63
<211> 1442

<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (933)
<223> n equals a,t,g, or c

<400> 63
catgaagatg tgaaaatatc atcttaacca gtttcattct atgaacataa tattctggca 60
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ccagtcacct gaggtcaggt ctgcacaaca ctaaattggg caataacata gaacatctag 180
gcagtcttga cagtcaacca gtgtaatcac taggggaagr aaaagtaggc ctaccctttt 240
acttattaac ttaagtaata aaaattgtat aaaaatatga atgttsgctg cagaggagcc 300
tttacatgca gataatttga agcagtcttt gaaaataaca aaaattattc catttaatga 360
agggtttgtt ttgtttagct tttctctttt attcagaaaa catacctgtg ccttttgaaa 420
gggcttaatc ccaaacaggt aatatgtgtg gatcaatcat ctctcctccc atgaaattaa 480
tcattcatgg taatatatta aggctggaac gtagctctta gtgacttaaa acatgacagt 540
aagcatttac actgttggaa ggtaatttca ttgctatgtt attaaaatga tgggaatcct 600
atttatacat ttatttattt atttatttac agaagattgg ttccttccag ttcaatttaa 660
cagcttcagt gaagttagta taatgataag aaaaattgac tgtagctatt attccaagtg 720
aaaatcatgc agctgagtcc tgctgcatcc tgggagcaaa gcattaattc aaatgaggag 780
tagtcagtcc tagcactgta gacgccgact ttaccaacca agatattgta tgtgtgtgac 840
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aaataatgat gttctattct gacctaatga attcctgtaa tgtgaatatt taaaataaaa 1380
gaattcaatt taaatgtata aaaaaaaaaa aaaaaaaact cggagggggg gcccggtacc 1440
ta 1442

<210> 64
<211> 1004
<212> DNA
<213> Homo sapiens

<400> 64
ccgggtcgac ccacgcgtcc ggggcgccca tgcatcacag ctgtgtccac aggatgcacg 60
atggccattg agaaatggat tttggagtca gaagacctgg gtgctgcatg cttaactcat 120
ctgggtcctt tggacaaatc acatcacctc tcatggcctc catatgttcc ttctgtgcat 180
gaaggatgat gttacttctt gcctctgcct tcctcatagg gacagtgtta ggatcaaaca 240
gatcatgtat gagtcagtgc tgtgggcacc ataaatcaca gaaagcccag aagacatcgt 300
catttattac agccccagtc aagtaaaagc ccatttaccc aggcacattg gttccaacag 360
taagcctttt tggctgatga aagctgtgta aagtttggtc tctggagaga agctgtttta 420
ttttttttaaa ccaagtctgt aaaaccttgg atgagaagct cttttagctc ttttatgttt 480
tgatcaataa tcaatgaagg cccaatataa gatctcctcc cccgaccgtg tatgcaacac 540
atttccaagg cccatccaca gcaactttgt tacttctgcc tgccgcatgc atggtttgaa 600
atttggcagc tcatattggt gtaaaaatca catatcactg taggctaaac tta[illegible]ctgc 660
acactcctcc atgtccactg agcatctgct gaagtctgct ttttc[illegible]tcat [illegible]gga 720
atgtaaagct catccatgtg tacattattc atgcatttac tttt[illegible] 780
attcaattaa agcaggaatt aaggctcaac tatcttactt tagca[illegible] 840
tgttacagtg agatgatttt tttctgtctg tcaaagttgt tt[illegible] 900
ggtctagaac atcatttaga gtaaattttc attttggagg [illegible] 960

tgtaggtatc tcctgtgaat agaggtttta aaaaaaaaaa aaaa 1004

<210> 65
<211> 1683
<212> DNA
<213> Homo sapiens

<400> 65
tgctctttct ggttccgctg ctgtgggccc cggctgcggt ccgggccggc ccagatgaag 60
accttagcca ccggaacaaa gaaccgccgg cgccggccag cagctgcagc cgcagcctgt 120
gstgtgcagg gccccgagcc ggccccgggtc gagaaaatat ttacaccagc agctccagtt 180
cataccaata aagaagatcc tgctacccaa actaatttgg gatttatcca tgcatttgtc 240
gctgccatat cagttattat tgtatctgaa ttgggtgata agacattttt tatagcagcc 300
atcatggcaa tgcgctataa ccgcctgacc gtgctggctg gtgcaatgct tgccttggga 360
ctaatgacat gcttgtcagt tttgtttggc tatgccacca cagtcatccc cagggtctat 420
acatactatg tttcaactgt attatttgcc atttttggca ttagaatgct tcgggaaggc 480
ttaaagatga gccctgatga gggtcaagag gaactggaag aagttcaagc tgaattaaag 540
aagaaagatg aagaatttca acgaaccaaa cttttaaatg gaccgggaga tgttgaaacg 600
ggtacaagca taacagtacc tcagaaaaag tggttgcatt ttatttcacc catttttgtt 660
caagctctta cattaacatt cttagcagaa tggggtgatc gctctcaact aactacaatt 720
gtattggcag ctagagagga cccctatggt gtagccgtgg gtggaactgt ggggcactgc 780
ctgtgcacgg gattggcagt aattggagga agaatgatag cacagaaaat ctctgtcaga 840
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agccctgatt ctggttttta acaagctgtt tgttcatcta tatttagttt aaaataggta 960
gtattatctt tctgtacata gtgtacatta caactaaaag tgatggaaaa atactgtatt 1020
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atggcacaac aagaactgtc tgccaggtca ttcttcctct ttttttttta attgggtagg 1500
acacccaata taaaaacagt caatatttga caatgtggaa ttaccaaatt aaaagagaat 1560
actatgaatg tattcatatt ttttctatat tgaataaaca atgtaacata gataacaata 1620
taaataaaag tggtatgacc aaaaaaaaaa aaaaacaaaa aaaaaaaaaa aaaaagggcg 1680
gcc 1683

<210> 66
<211> 1441
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (1362)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1364)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1421)

<223> n equals a,t,g, or c

<400> 66
aagttggttt cggctgcaga ggggaaggcg gctaccagtg taaagccaga gctgaggttc 60
ttgatagtcc acaatgggtg aaccacagca agtgagtgca cttccaccac ctccaatgca 120
atatatcaag gaatatacgg atgaaaatat tcaagaaggc ttagctccca agcctccccc 180
tccaataaaa gacagttaca tgatgtttgg caatcagttc caatgtgatg atcttatcat 240
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agaactgaga aaacttaata tgtctatcct tattaatttc ttggaccttt tagatatttt 360
aataaggagc cctgggagta taaaacgaga agagaaacta gaagatctta agctgctttt 420
tgtacacgtg catcatctta taaatgaata ccgaccccac caagcaagag agaccttgag 480
agtcatgatg gaggtccaga aacgtcaacg gcttgaaaca gctgagagat ttcaaaagca 540
cctggaacga gtaattgaaa tgattcagaa ttgcttggct tctttgcctg atgatttgcc 600
tcattcagaa gcaggaatgc agagtaaaaa ctgaaccaat ggatgctgat gatagcaaca 660
attgtactgg acagaatgaa catcaaagag aaaattcagg tcataggaga gatcagatta 720
tagagaaaga tgctgccttg tgtgtcctaa ttgatgagat gaatgaaaga ccatgaaaga 780
tgtttctttt tctttttttc cttttgataa tagcatcata tattagttca ttttcttttg 840
gacagtctta agagaagttt cactaaaaat gtaaacagct ttaatcttga ctccaaattt 900
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tcgtctttga aaaggggatt tagcatttgc tttaagaatg atagataaat ggatattaag 1140
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tccaaaaagt agcataacat gttgatagag aggagcccag tagagttata aaatagaaac 1260
ttcatttttt cctcatgact gcttctgtaa acccactagc tcagtctttt ctcgctatcc 1320
tgaatggact cttgcaggga agtccccata aatgttgttt tntngccagt cactccaggg 1380
gaataagtcc tttggggcac tttaaagtta cagacattaa ntttaagtaa ttaagatggc 1440
c 1441

<210> 67
<211> 622
<212> DNA
<213> Homo sapiens

<400> 67
gcaattcggc acgaggggcc ctctcctctg ctgactcttg ccatttttcc aggcctcccc 60
tcagtgagga gaccaggcga tgggagacag gcatggtgct gcttctgctg ctccagagaa 120
accctgggac acctttgttc tgcttggttt tctgggctgg gctcaggaaa cctgcccagt 180
tcaggcctat attgggtcca agctgccccт gtgctgcttc tgtcaagcga ggtgtggaca 240
ttccaagttc gtaagcatga acaaaagaaa agaggaaccc agcagatgta acagaactga 300
ctccagttgt gtagagtttt gctaaactgt ttatcccctt ttgctgtggt ttacattaat 360
ggcaatagtt agccaggtgt ggggaatgag agtgcattgc tcgatagggt ctgatgaact 420
gggagtaacc caccattgca attggggatt gttttgcaag gaaatagtat ttttatgtgg 480
gggaccagca aaatctctac attagtgtaa aatttcaaat agttgtttta tcgttggttt 540
ggtttaccaa caaaaaaaaa aaaaaaaaaa aaaaaaaaaa ctcgaggggg ggcccgtacc 600
caatagccct ctcatgtatc gt 622

<210> 68
<211> 616
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
equals a,t,g, or c

<400> 68
gncccaacgc aattaatggg rgttagctma cycattaggc acccaaggct ttaaacttta 60
tgcttccggc tcgtatgttg tgtggaattg tgagcggata acaatttcac acaggaaaca 120
gctatgacca tgattacgcc aagctcgaaa ttaaccctca ctaaagggaa caaaagctgg 180
agctccaccg cggtggcggc cgctctagaa ctagtggatc ccccgggctg caggaattcc 240
ccccccccc cccacacccc cttcagctat gcttttggag tcctggatgg gaatctgggg 300
ggagagagga aggacaggtc aggtctcccc cagccccttc tgctcctgtc tcctcgtgtc 360
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ctttacctgc ttcgtatcct ttccctgctg atgtggctga cccctctccc acccctccct 480
gcaggcggct ggccaggtgg gcaggtgcca gccggagctg taaatagasc gtgcgctttt 540
gtgctggttt gtgcgtgtgc tgtatttctg tgttttgata gaagtcacac aaaaaaaaaa 600
aaaaaggatc cctcga 616

<210> 69
<211> 1019
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (884)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (922)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (939)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (965)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1003)
<223> n equals a,t,g, or c

<400> 69
ggcgtccagg tccgctcggt aaccgtttcc cgcgcgcccg gccccgactc cggggtaaag 60
agccccggag cggagcagcg ctggccgcgt gccgcctccg gagccggcag cccccatggc 120
tgggggttat ggagtgatgg gtgacgatgg ttctattgat tatactgttc acgaagcctg 180
gaatgaagcc accaatgttt acttgatagt tatccttgtt agcttcggtc tcttcatgta 240
tgccaaaagg aacaaaagga gaattatgag gatattcagt gtgccaccta cagaggaaac 300
tttgtcagag cccaactttt atgacacgat aagcaagatt cgtttaagac aacaactgga 360
aatgtattcc atttcaagaa agtacgacta tcagcagcca caaaaccaag ctgacagtgg 420
gcaactctca ttggaatgaa acctcagaaa aagagcaaca gaagtaattg ttgcaagctt 480
ctgattcttt ctactaaatc atgaacagct ttaaaaacat ttctgtctgc ttt tatttg 540
tttacttgta acttttcccc aattgttctg tgcattgttt tgccttttt[illegible] tgat 600
ccaagtggct caaaaggcct tgacacaggg aacctgcaca tatccac[illegible] aaa 660
agcgatggtg acttgacctt gccaagacct gtgattcctt caggat[illegible] 720

ataaaaacac atcttgggaa gtgggaatcc tggagtttat gccatttgca atattaaaaa 780
ataaaaatgc aagttattat ttcaataata acttcctgtt tcattgtatt ctgtgagtga 840
taagtgtcag atcaataaca gattaatttg ttgttaacag ctcnttttt ttttttttt 900
tttggagaca ggagtctggt tngcccagac ttggagtgnc agtgggccaa atcctctggc 960
tcaantggca aacttccaac ctccccgggg tttaaacgga ttnctccctg gccacagcc 1019

<210> 70
<211> 831
<212> DNA
<213> Homo sapiens

<400> 70
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tatttgtcag ataatagaca tttgggttat tgctgtcttt tggctattat gagtgttata 120
aatatttgtg cacaagtatt tgtgtagaca tgtttgcatt tctcttgggt atatacctag 180
gagtgaaatt gctggataat atgtttaact atttgaggac tgatagacta ctttgtaaag 240
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gcaaagcatt taataagcag caagagttaa accacgttgg tccaagtgaa ctgaaagcag 360
acttctgtgt tacatgtgta tgagttactg aacatgttcc ataatacagg agtgtgagca 420
cactaacagg taagtgcagg aaamcaagaa gaaatatttt cagagtatag tcaaaagtac 480
actgagcatg ggagaattgt tttgacattt tgctcaaaac tatttctgaa gaaaattcaa 540
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atatgttcgt tcagatgacc ttgaagtgtt ttttcagact tatctgaact tgagatctga 660
actgaatttt tattagaaac tgttaaagcc tctggcattg aaggttagtt cataattggt 720
gagttctgaa tcacttcatt tcckgcagtg gttcctgaga gaatcttagt tmaaaggact 780
gcccccgcca acccctgccc cgccaaaaaa aaaaaaaaaa aaaaaactcg a 831

<210> 71
<211> 750
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (734)
<223> n equals a,t,g, or c

<400> 71
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gcagggtgtc ccacatgatg cagcctgtcc tcatatgggg actctgagct ctgagactcc 120
ctgtgtgaga tgtttgggtg cagagctgtg aagacacaga aggaaacgtt gccgtctgca 180
ccaggctccc caccgttggt ggccctgttt tccgtggccc tgtggcctgt ggccctgtct 240
aacgaggcca caccacattc atgtggacaa gcaccaggag ctccgggtca gatgagaaca 300
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cctcggtgag gatgacacca gcatcccctt gaccctccaa ggtctcctgt gacattgccc 420
cagaggctct tgctgtgggg ccgtccagtt tatgtggagt gacctgcacc ctgagcacag 480
cccaacaktt ggccacacct tgggggcccg aggggctgag ttctacccag agcggctgga 540
ggctcacaag ggattttccc accttggagg gagccaagtt cccctggggg gcaggtgggc 600
tgctcagctc tgaaagacct cagtgccgtg gagtgcgctc tggaggaagg gtactgagcc 660
gattccctga cagtgactgt aataaagatg gctaaataga gaaaaaaaaa aaaaaaaaaa 720
aaaaaaaaaa tagnaggggg tcccgtaccg 750

<210> 72
<211> 714
<212> DNA

<213> Homo sapiens

<400> 72
gaattcggca cgaggaggag ttattcaggc ctccgccagc ttcaaggccc tggggatggt 60
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gatggcaaaa gagcccagaa cctattggaa ctgacaaaat caagtcacgg cgcctacaaa 180
gatgaggggc agattctggc tgccttttaa tttcgtcctt cacctgatat ctgtgccaga 240
gaatgtggca tggttcagtc ttccaggagt tctgctacag agaagagagt aacccccatc 300
catcatggcc aaagcaccca gtcaggctcc gctctggatc cagcccgaca aatgcaaccc 360
ttgaataggg tttgtgcaag caaactggat gacgaccgaa gaaaccctgt cgcttctgag 420
aagacaccca atccaagaat gaaagcatca ggttcaatac ctaggaactc ctgtagaggg 480
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cagccaggtg tggtgggtca tgcctgtaat ctcagcaatt tgggaggcca aggcaggatc 600
tcagcaattt gggaggcgaa ggcaggcaga tcacttgagc ctaggagttc aagaccagct 660
tgggcaacat agcaagaccc tgcctatacc aaaaaaaaaa aaaaaaaact cgta 714

<210> 73
<211> 1405
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (8)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (35)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (59)
<223> n equals a,t,g, or c

<400> 73
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aactgtgaag aacccccaaa aaacttccca cttcctggga ggccagccca caggaacagg 120
gaacaatatt tatttgggtc tcttcagttc ccccttttgag aacaacatta aatacatgtt 180
agctggggct cccagggcat tctccttccc acagtagtgc ggccaaattc ccagtctggc 240
cagtctcttt gttgagactg aatagaagga ctgcaggttt ttttggagga tgagataatt 300
tttcctcgca ggcatttttc ccttgccttc cttatgcatg aatggtccct ttgaatatta 360
tttccaaaag tgagagctaa gacaaagtca tcaaaaagag aggataacag aaggtggggg 420
cgggggcggg gtgcagtggg gtagggttac ctgttaattg ctgagactca gatgaaagtc 480
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ctgcttgttc taaactacac cttaggattt tttcttcttt ccaaaacatt ccattgattt 600
tataaagact ttctatagag aggctttcac ttttgagttc tttgagttta aagattgctt 660
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ctttatattt caagctcttt atttaaacat tgttggaata tgtggcataa gccttgtttc 1320
atttatttaa taaactggag taatatataa taataaaaaa aaaaaaaaaa aactcgaggg 1380
ggggcccggt acccaatcgc cctat 1405

<210> 74
<211> 907
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (455)
<223> n equals a,t,g, or c

<400> 74
gggtcgaccc acgcgtccgg caaagatcat ttcagtctcg ggcttcttcg tgggaacttg 60
acttgccggg tagctccccc tggggttcag atctctgttc attgtttctc ttcaagccct 120
gggaagtgcc atgttatctg gaaagctttc cctaacatgt tctgtctgca tttatacttc 180
acccatgtgc ccctcaacta ttcatcatag ccctagtccc accataatga aaatgtctct 240
cattattttt ctggctggcc cacgagcctg caagtcctta taggcgccaa ctaagtatca 300
ttcatccctg gatgctctcc cactagacgt ttattgaatg aagagtggag gaatgaatga 360
agcaacgatg gctttctctg tgctcatcct tccagtgttc tacgcacaga ttaggaacaa 420
gagtttcctt tgtctttctg acattctycc attantcctc atcctcctct tttgatagac 480
tcaaggttta cccaattggt gaatctctct tctgagcctt ctcctaaact aatttgtccc 540
cagaatagca ccccttctcc ctctctgtcc ttaccaacac atgcttctga cagtccaggt 600
tccacctctg aaatgtcagc taaaactctt ctcattcagg cagtgttccc tgtccagaaa 660
agaggcagca ctttctctct tgctctattt gaattaaaca tgcagttgcc aggagtcacc 720
tgaattcaca ctctacagca tactctttct tccccccttga ttcaagcatg atgtaaaatg 780
ttatacattt tttttcaagt tgtaaaagta ttaattcatt tgcatcgatg acttatcttt 840
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ggcggcc 907

<210> 75
<211> 687
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (461)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (481)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (534)
<223> n equals a,t,g, or c

<400> 75
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agaggcagca cttggcaccc ttaatcaccc aaattaagca attattctga tcc

gaaatgaatt ggtatcatga gaacaaagag gcaacatgca attgccaaat atttggccta 180
tattttattg tttcctttct ttctccagta ctggcagcag cccatgatgc taagaaatat 240
cccgtttggt tatgaagtta atgtggagat taaaagtcat tccctgttct acccacaccc 300
tttttcttgt gtatagcatg tgactgagct gattggaagg catatagccc agtggccaag 360
cacttgggcc tcagtgtgat ggctgacaca tgtttctgac tctgtccatt tctatwttgt 420
tgtggacaag ccttggcttt ctcagctgtc aaatgggggt nacaacagct ctacatatag 480
ncctgtagca attaaatgaa agcatttagg gccaggcatg gtggcttatg gcgntggtcc 540
cagcacttag ggaggccaag gcaggacaaa gtgggctctt gtctttgagc cctagagttt 600
gagaccagcc tgggcaacat agtgaggccc tgtctctaaa aaaaaaaaaa aaaaaaaaac 660
tcgaggggg gcccgtaccc aatcgcc 687

<210> 76
<211> 792
<212> DNA
<213> Homo sapiens

<400> 76
gaattcggca cgaggtgaag cacactcaca tactcaaatg cacacacact catacacaca 60
gccccacacg ctagcacata cactcccttc actccgcccc tcttgtaagg cgatttcttc 120
ttcccaggac aggagctaga ggtgcagcct gggaccactc agccaagaag ccaagggcca 180
ggcatgcccg ggcctggagc actttattca tcttttacgt ctttttatta cacattctcg 240
aatcaccagc tcctccttgc cttgcttctc ctgggtttca ttgcctcttg cagtttcttc 300
ctctctcgag tgtttctaac tttttccacc caattatgga aaaagtaaga accgagaaca 360
gcgaaaacaa ccaaaacaaa atctatagct atttctcatt gaaatcctgg aagaattttg 420
ggtttycect tcgatttctc tcacccactc acgcattcac caattatgta tttgtttact 480
caatgagtgc agctcaggcc gagggtgcca gcctccacgg gatgaggggc tagacactct 540
gatttcaccc cgacacctgc tgggtgcaag scgctcagtc tgcagccagc tctaggtccc 600
gcccctttgc gttgggctgc gggtgggcgg ggctgcttgg cctgcccaga ctcgccagga 660
aagacatgct gctgcggacc aatcagagtg gcccaagctg ggaggaggcc ttgccccgcc 720
ctcccctgcc ccgcccactt ggcgctggga ataaccacgt ggaaacccaa ctccgaggtc 780
tctggcgctc ga 792

<210> 77
<211> 756
<212> DNA
<213> Homo sapiens

<400> 77
tcgagtaccc tgaagtcctc ctgctgttgt ttccaaccaa gaaagttttc catgagtaag 60
tctgagcaat gccgagctgc ttgcccagct gccctggagc aggagctatc actgggcagg 120
ggctggtggg ggtgggcaac agaagggata ggaagccaga ttcacccagt cagtccccca 180
gcatcaccaa agcaaagccc ctccctcctc caaagcatgt gggataggtg taatagttac 240
acacatggtt ctttgcagtg ggacagactg aggcctccac ctgttctgcc accttctatc 300
tacacaatca ggacatgttc tcaaaggtta tttgctgcag cccagtccty ttcctattct 360
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ccaagcctct caagcctgct gttccaccag agcagcccag cytgcacact gtcagcytgg 480
cctctgtcta ggtacgccca gccaggctca gcgctgctga ccacaccacc aagactgcag 540
agaggctgag caaacagccc tgctgggggc tctcacacct catcaccact taccactttg 600
agggaccaag gcaggccagg agacatccat cttgagaaat gccaggcctg ggccaatcat 660
gtgacagcta ctttcccagt actctccctc cctctctcgc tctttcccct ctctccagaa 720
cttcttgagg agtacaaggc ccctcgtgcc gaattc 756

<210> 78
<211> 751
<212> DNA

<213> Homo sapiens

<220>
<221> SITE
<222> (750)
<223> n equals a,t,g, or c

<400> 78
gcggccatgg tgaccatggt gacagggtcc cagccagaaa ccacaatggg atggaaactc 60
ctggggctgc tgtcagcagc tgggagacac agcgctgggg gagaccaggc attccccagg 120
cccaagggag aagcagagtc ggcctcgcct gagccagacg caggccttgg gtttaccctc 180
catggaccag acgtaaagtc taatggtgac atgagatttt taatgtcttt acatctgcag 240
atgtacacgt cagcaaaatt gcatcacaca aacctcactg caggcccagg ctttcctctt 300
tccaggtttc accaacctcc tccctccgtc ttggctgcct gtccctccac caatcagctc 360
tcacctgccc caggtgaccc gcgttaacag tggcacatga atttctcaca ttcatacaca 420
cataaatgca cgtctcttca ggcaaataca catttggaaa ggattttcct cctggcttgt 480
cctatgaacg taagaacgtg atctgcacgt ttttctgaga gttgctcttt ctcctaaccc 540
actcctccct gtgccccacc catgtggcca gccctccgtg tccaccatcc tctgctccct 600
sccagggctt tgctccagga acgaagtccc aggcagcctc ctaggacaca agtttctgtt 660
ccttctgctc ccttggggtt tcctcgtaga atgaagactc ccagtggagt tactgggtca 720
aagaagacct gtatttttag tttccctcgn c 751

<210> 79
<211> 1411
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (541)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1324)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1370)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1395)
<223> n equals a,t,g, or c

<400> 79
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agcacatttg tgatatgttg aaaagcatct ctcttggcaa ccaatctatg tttgaggaag 180
attgggtaat gctgatgtat tccattcatg aaactgtatt tgatacataa tcctattatt 240
aattcgtatg cttagtca c aggaaatc aaaataatgt tttgaagttc ttatttgagc 300
aatatggcct agtttta gttgttttgt ttttaagtga ctgtggttta 360
aagcacaaat gagactt ctctctgtga ttattgttgc tattaaattc 420
tgaactgtat aggagc taaaaatgga aattcatgaa acataaatgg 480
tatcaag tgttg aaagcagaaa ttaagataat aattgagttc 540

naattcgcct ctccgcattg cctattgata cactttacta atcatgaaat tctaacctaa 600
aaggaaaaca ttttcctgct tgtcttagaa gaaagtggaa taattccact gattgtgata 660
atggtttcaa tttctacaca atataaatat ccagtataaa ggaaagcgtt aagtcggtaa 720
gctagaggat tgtraatatc ttttatgtcc tctagataaa acacccgatt aacagatgtt 780
aaaccttta atgttttgat ttgctttaaa aatggccttc ctacacatta gctccagcta 840
aaaagacaca ttggagagct tagaggataa gtctctggag magaatttat cacacacaaa 900
agttacacca acagaatacc aagcagaatg atgaggacct gtaaaatacc ttgtgcccta 960
ttaaaaaaaa aaaaaaaaaa aaaagccagt arctgaatcc attttgattt ttggttgagt 1020
ttcctacaca aagaagaaaa taactgagaa tctggaatgt tgtagtccat cctttaaaga 1080
gtaagaaagt agcagttaat gctagtaacc gtgaattagg caccactgaa agcacatccc 1140
gaatttcttt aacaacaaca ttttatagtg aacactacaa gtttttatat ttaaaawtta 1200
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gacnatgtaa taagccttat aatagtataa ccgtccagga gatatatatn tatatatcca 1380
ccccccccca cgggnacaca gattttacca a 1411

<210> 80
<211> 866
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (14)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (27)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (33)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (105)
<223> n equals a,t,g, or c

<400> 80
cctggcttgc tggncaagcc ttggtgncca tgntgaacaa gttttgtgga agttctgggg 60
agactccaag aactaccagg aacagggata cgagtgccag gctgnatctc ttgctcctct 120
gcagagtcag caggcttctt ctcagagatg acagaagacg agttggtggt gctgcagcag 180
atgttctttg gcatcatcat ctgtgcactg gccacgctgg ctgctaaggg cgacttggtg 240
ttcaccgcca tcttcattgg ggctgtggcg gccatgactg gctactggtt gtcagagcgc 300
agtgaccgtg tgctggaggg cttcatcaag ggcagataat cgcggccacc acctgtagga 360
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agcttggttt atttttgaga gtggggtaag caccctacc tgccttacag agcagcccag 480
gtacccaggc ccgggcagac aaggcccctg gggtaaaaag tagccctgaa ggtggatacc 540
atgagctctt cacctggcgg ggactggcag gcttcacaat gtgtgaattt caaaagtttt 600
tccttaatgg tggctgctag agctttggcc cctgcttagg attaggtggt cctcacaggg 660
gtggggccat cacagctccc tcctgccagc tgcatgctgc cagttcctgt tctgtgttca 720
ctacatcccc acaccccatt gccacttatt tattcatctc aggaaataaa gaaaggtctt 780
ttaaagttaa aaaaaaaaaa aaaaaaaaaa aaaaaaactc gaggggggggc ccgtacccaa 840
tcccctatg atgtagtcgt attaca 866

<210> 81
<211> 2078
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (1177)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1187)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (2057)
<223> n equals a,t,g, or c

<400> 81
ggcacgagga gttgtgcaga tacctggctg agagctggct caccttccag attcacctgc 60
aggagctgct gcagtacaag aggcagaatc cagctcagtt ctgcgttcga gtctgctctg 120
gctgtgctgt gttggctgtg ttgggacact atgttccagg gattatgatt tcctacattg 180
tcttgttgag tatcctgctg tggcccctgg tggtttatca tgagctgatc cagaggatgt 240
acactcgcct ggagcccctg ctcatgcagc tggactacag catgaaggca gaagccaatg 300
cyctgcatca caaacacgac aagaggaagc gtcaggggaa gaatgcaccc ccaggaggtg 360
atgagccact ggmagagaca gagagtgaaa gcgaggcaga gctggctggc ttctccccag 420
tggtggatgt gaagaaaaca gcattggcct tggccattta cagactcaga gctgtcagat 480
gaggaggctt ctatcttgga gagtggtggc ttctccgtat cccgggccac aactccgcag 540
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ctaagccggg acctagggga gggagaggag ggagagctgg cccctcccga agacctacta 660
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gcagctaagg aaaccttgtt gcggctctca tccccctcc actttgtgaa cacgcacttc 780
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cttccttact gctcctctgg gtgatccaag tgtagtggga cc[illegible] gtcaggaa 1980
gtggacacta acatctgtgc aggtgttgac ttgaaaaata aa[illegible] gttacaaa 2040
aaaaaaaaaa aaaattnctg cggtccgcaa gggaattc 2078

<210> 82
<211> 1064
<212> DNA
<213> Homo sapiens

<400> 82
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tgtgtttacg gctgttgcta gaaattgcag acaacccgga ggcggtcgat gtgaaagatg 120
ccaaaggaca aacaccactg atgcttgcag tagcatatgg acatattgac gctgtttcat 180
tgttacttga aaaggaagcc aacgtrgaca ctgttgacat cctaggatgc acagctttac 240
acagaggggt atgtacatct ttctcagctc tagtcaagca atttttttaa tgagctgttt 300
tctttttttag caaacaatta caaagggcct actttgattg gatttttagc aaaaaatgtt 360
tagcaaaaat tgtttcctaa tacaaccaat taaccttatt cagtccaaaa gaaattacaa 420
aatccttggc aaaggcaaaa taatggaagg ttttgctctt aagatttcat gttagattgt 480
gataatagat gcatgaacac ctactgctgg tgaaattggt tctgctttct gactacaaaa 540
tacaagtata tcatagaaaa tttgcagaat attttttttt aaagcccaga gaagaaaatc 600
acaatcacca gtaatcatac ctcctggaga taaccactat ttgatgtata ttatctccaa 660
tctttttttct atatatagat ttgttttaga ttttaaaaag agaatactga agatatcatt 720
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tcctgtgggc aattatttgc acacatctgt tgaagtgttt ggtttttttt tttttaatct 960
cactcttatc acccaggttg cagtgagccg agatcacacc actgcattcc agcctgggtg 1020
acacagcgag actccatctc aaaaaaaaaa aaaaaaaaac tcga 1064

<210> 83
<211> 1126
<212> DNA
<213> Homo sapiens

<400> 83
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tgcggtccgg gccggcccag atgaagacct yagccaccgg aacaaagaac cgccggcgcc 120
ggcccagcag ctgcagccgc agcctgtggc tgtgcagggc cccgagccgg cccgggtcga 180
ggacccctat ggtgtagccg tgggtggaac tgtggggcac tgcctgtgca cgggattggc 240
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aggcatcgtt tttttggcgt ttgcattttc tgcactattt ataagccctg attctggttt 360
ttaacaagct gtttgttcat ctatatttag tttaaaatag gtagtattat ctttctgtac 420
atagtgtaca ttacaactaa aagtgatgga aaaatactgt attttgtagc actgattttg 480
tgagtttgac ccattattat gtctgagata taatcattga ttctatttgt aacaaggagt 540
tttaaaagaa acctgacttc taagtgtggg ttttttcttct ctccaacata attatgttaa 600
tatggtcctc atttttcttt tggtgcagaa ccgttgtgca gtggggtcta ccatgcaatt 660
ttctttcagc actgacccct ttttaaggaa tacaaatttt ctccttcatc acttaggtgt 720
tttaagatgt ttaccttaaa gtttttcttg gggaaagaat gaattaattt ctatttctta 780
aaacatttcc ctgagccagt aaacagtagt ttaatcattg gtcttttcaa aactaggtgt 840
ttaaaaaaag agacatatat gatattgctg ttatatcaat aacatggcac aacaagaact 900
gtctgccagg tcattcttcc tctttttttt ttaattgggt aggacaccca atataaaaac 960
agtcaatatt tgacaatgtc gaattaccaa attaaaagag aatactatga atgtattcat 1020
atttttttcta tattgaataa acaatgtaac atagataaca atataaataa aagtggtatg 1080
accaaaaaaa aaaaaaaaca aaaaaaaaaa aaaaaaaagg gcggcc 1126

<210> 84
<211> 30
<212> PRT

<213> Homo sapiens

<220>
<221> SITE
<222> (30)
<223> Xaa equals stop translation

<400> 84
Met Pro Ala Leu Ser Met Ala Leu Thr Met Leu Gly Cys Tyr Ala Ile
1 5 10 15

Ala Ile Leu Leu Phe Val Thr Leu Val Arg Lys Pro Ala Xaa
20 25 30

<210> 85
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (34)
<223> Xaa equals stop translation

<400> 85
Met Phe Cys Ile Ser Leu Ser Phe Phe Asn Leu Pro Glu Tyr Ser Pro
1 5 10 15

Cys Ser Leu Leu Ser Val Gln Glu Leu Val Pro Gln Phe Phe Tyr Val
20 25 30

Val Xaa

<210> 86
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 86
Met Lys Val Ala Val Arg Gly Lys Gln Arg Glu Cys Arg Asp Arg Ile
1 5 10 15

Leu Gly Lys Lys Thr Lys Ala Trp Thr Gln Arg Arg Arg Ser Lys Cys
20 25 30

Gly Ser Gly Tyr Lys Val Arg Val Ser Val Gln Glu Val Asn Lys Val
35 40 45

Ser Thr Arg Lys Ser Xaa Arg Ser Arg Lys Pro Ala Phe Gly Asp
55 60

Arg
65

<210> 87
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (27)
<223> Xaa equals stop translation

<400> 87
Met Leu Leu Phe Phe Phe Trp Thr Leu Phe Arg Glu Ser Val Asp His
1 5 10 15

Asn Asn Ser Asp Thr Phe Phe Ser Gly Pro Xaa
20 25

<210> 88
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (49)
<223> Xaa equals stop translation

<400> 88
Met Leu Ser Lys Ser Ser Lys Met Val Ser Val Lys Arg Ala Asp Pro
1 5 10 15

Gly Ser Leu Gly Phe Thr Phe Leu Leu Ser Ser Leu Pro Lys Cys Thr
20 25 30

Val Gly Val Ser Arg Gly Arg Pro Thr Cys Thr Ser Cys Ser Asp Gly
35 40 45

Xaa

<210> 89
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (33)
<223> Xaa equals stop translation

<400> 89

Met Ser Met Asp Leu Ala Asn Leu Tyr Leu Leu Phe Ile Val His Arg
1 5 10 15

Phe Leu Ile Phe Phe Ile Pro Val Ser Phe Lys Leu Pro Ser Phe Glu
20 25 30

Xaa

<210> 90
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (23)
<223> Xaa equals stop translation

<400> 90
Met Tyr Leu Val Phe Cys Leu Ser Cys Val Ser Asn Gln Gly Pro His
1 5 10 15

Ser Pro Val Gly Thr Trp Xaa
20

<210> 91
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (55)
<223> Xaa equals stop translation

<400> 91
Met Ser Asn Val Val Phe Ser Leu Lys Ala Val Met Trp Val Leu Phe
1 5 10 15

Tyr Cys Leu Phe Val Cys Cys Cys Ile Leu Phe Ser Leu Leu Phe Ala
20 25 30

Leu Gln Asn Ala Leu Gly Lys Gly Trp Phe Leu Ser Leu Leu Val Cys
35 40 45

Val Phe Phe Phe Phe Phe Xaa
50 55

<210> 92
<211> 39
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (39)
<223> Xaa equals stop translation

<400> 92
Met Ser Thr Val Lys Gln Ile Val Met Gly Leu Tyr Phe Val Tyr Xaa
1 5 10 15

Tyr Val Cys Phe Phe Tyr Ser Thr Phe Cys Gly Ser Ser Val Leu Leu
20 25 30

Val Ala Ser Ser Leu Leu Xaa
35

<210> 93
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (53)
<223> Xaa equals stop translation

<400> 93
Met Cys Leu Phe Phe Glu Asn Val Thr Leu Leu Phe Val Ile Val Leu
1 5 10 15

His Phe Ser Ala Phe Arg Pro Leu Tyr Phe His Lys Thr Pro Lys Thr
20 25 30

Ala Phe Asn Tyr Ile Ile Met Ser Val Phe Leu Asp Thr Asn Phe Cys
35 40 45

Ser Arg Met Thr Xaa
50

<210> 94
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (337)
<223> Xaa equals stop translation

<400> 94
Met Ile Ser Tyr Leu Leu Ser Ile Leu Leu Trp Pro Leu Val
1 10 15

Val Tyr His Glu Leu Ile Gln Arg Met Tyr Thr Arg Leu Glu Pro Leu
20 25 30

Leu Met Gln Leu Asp Tyr Ser Met Lys Ala Glu Ala Asn Ala Leu His
35 40 45

His Lys His Asp Lys Arg Lys Arg Gln Gly Lys Asn Ala Pro Pro Gly
50 55 60

Gly Asp Glu Pro Leu Ala Glu Thr Glu Ser Glu Ser Glu Ala Glu Leu
65 70 75 80

Ala Gly Phe Ser Pro Val Val Asp Val Lys Lys Thr Ala Leu Ala Leu
85 90 95

Ala Ile Thr Asp Ser Glu Leu Ser Asp Glu Glu Ala Ser Ile Leu Glu
100 105 110

Ser Gly Gly Phe Ser Val Ser Arg Ala Thr Thr Pro Gln Leu Thr Asp
115 120 125

Val Ser Glu Asp Leu Asp Gln Gln Ser Leu Pro Ser Glu Pro Glu Glu
130 135 140

Thr Leu Ser Arg Asp Leu Gly Glu Gly Glu Glu Gly Glu Leu Ala Pro
145 150 155 160

Pro Glu Asp Leu Leu Gly Arg Pro Gln Ala Leu Ser Arg Gln Ala Leu
165 170 175

Asp Ser Glu Glu Glu Glu Glu Asp Val Ala Ala Lys Glu Thr Leu Leu
180 185 190

Arg Leu Ser Ser Pro Leu His Phe Val Asn Thr His Phe Asn Gly Ala
195 200 205

Gly Ser Pro Gln Asp Gly Val Lys Cys Ser Pro Gly Gly Pro Val Glu
210 215 220

Thr Leu Ser Pro Glu Thr Val Ser Gly Gly Leu Thr Ala Leu Pro Gly
225 230 235 240

Thr Leu Ser Pro Pro Leu Cys Leu Val Gly Ser Asp Pro Ala Pro Ser
245 250 255

Pro Ser Ile Leu Pro Pro Val Pro Gln Asp Ser Pro Gln Pro Leu Pro
260 265 270

Ala Pro Glu Glu Glu Glu Ala Leu Thr Thr Glu Asp Phe Glu Leu Leu
275 280 285

Asp Gln Gly Glu Leu Glu Gln Leu Asn Ala Glu Leu Gly Leu Glu Pro
290 295 300

Glu Thr Pro Pro Lys Pro Pro Asp Ala Pro Pro Leu Gly Pro Asp Ile
305 310 315 320

His Ser Leu Val Gln Ser Asp Gln Glu Ala Gln Ala Val Ala Glu Pro

325 330 335

Xaa

<210> 95
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (49)
<223> Xaa equals stop translation

<400> 95
Met Leu Pro Tyr Ser Leu Pro Phe His Ile Ser Cys Thr Ser Ser Leu
1 5 10 15

Ser His His Leu His Pro His Leu Leu Ser Leu Leu Leu Ser Phe Ser
20 25 30

Pro Lys Gly Val Thr Ala Asp Val Lys Ile Ser Leu Met Met Ala Lys
35 40 45

Xaa

<210> 96
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (38)
<223> Xaa equals stop translation

<400> 96
Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Thr Ala Phe Ala
1 5 10 15

Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly Asp Lys Pro Gly
20 25 30

Ala Asp Thr Gly Arg Xaa
35

<210> 97
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

50

<222> (29)
<223> Xaa equals stop translation

<400> 97
Met Leu Phe Lys Leu Phe Phe Ser Leu Ile Leu Phe Ser Phe Val Val
1 5 10 15

Ser Cys Ile Phe Ser Val Ser Ile Asn Ile Pro Leu Xaa
20 25

<210> 98
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (36)
<223> Xaa equals stop translation

<400> 98
Met Pro Phe Met Phe Leu Ser Leu Pro Arg Asp Thr Phe Leu Met Leu
1 5 10 15

Glu Leu Val Leu Gly Thr Phe Thr Cys Asn Gly Ser Phe Phe Ile His
20 25 30

Lys Ala Ser Xaa
35

<210> 99
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (182)
<223> Xaa equals stop translation

<400> 99
Met Ala Ala Leu Cys Arg Thr Arg Ala Val Ala Ala Glu Ser His Phe
1 5 10 15

Leu Arg Val Phe Leu Phe Phe Arg Pro Phe Arg Gly Val Gly Thr Glu
20 25 30

Ser Gly Ser Glu Ser Gly Ser Ser Asn Ala Lys Glu Pro Lys Thr Arg
35 40 45

Ala Gly Gly Phe Ala Ser Ala Leu Glu Arg His Ser Glu Leu Leu Gln
50 60

Lys Gly Ser Pro Lys [illegible] Phe Ala Ser Met Leu Arg His
65 75 80

Ser Pro Leu Thr Gln Met Gly Pro Ala Lys Asp Lys Leu Val Ile Gly
85 90 95

Arg Ile Phe His Ile Val Glu Asn Asp Leu Tyr Ile Asp Phe Gly Gly
100 105 110

Lys Phe His Cys Val Cys Arg Arg Pro Glu Val Asp Gly Glu Lys Tyr
115 120 125

Gln Lys Gly Thr Arg Val Arg Leu Arg Leu Leu Asp Leu Glu Leu Thr
130 135 140

Ser Arg Phe Leu Gly Ala Thr Thr Asp Thr Thr Val Leu Glu Ala Asn
145 150 155 160

Ala Val Leu Leu Gly Ile Gln Glu Ser Lys Asp Ser Arg Ser Lys Glu
165 170 175

Glu His His Glu Lys Xaa
180

<210> 100
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (84)
<223> Xaa equals stop translation

<400> 100
Met Asn Val Leu Val Tyr Ser Asp Lys Glu Lys Lys Asn Gln Lys Ser
1 5 10 15

Gly Leu Asn Leu Ile Val Phe Ile Ile Lys Ile Leu Lys Met Thr Leu
20 25 30

Ile Ala Arg Lys Thr Gly Trp Gly Ile Ser Pro Leu Leu Ser Val Thr
35 40 45

Met Arg Ile Ile Pro Ala Leu Val Phe Asn Thr Arg Leu Pro Thr Phe
50 55 60

Ile Ile Ser Leu Ile Phe Leu Leu Phe Ser Cys Ile Cys Glu Leu Val
65 70 75 80

Gln Glu Cys Xaa

<210> 101
<211> 25
<212> PRT
<213> Homo sapiens

<221> SITE
<222> (25)
<223> Xaa equals stop translation

<400> 101
Met Gln Val Leu Met Leu Ala His Phe Leu Ile Leu Leu Glu His Val
1 5 10 15

Gln Gly Arg Cys Ser Asp Asn Asn Xaa
20 25

<210> 102
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (32)
<223> Xaa equals stop translation

<400> 102
Met Asp Cys Met Cys Ile Tyr Met Phe Leu Ile Ile Leu Ile Asn Val
1 5 10 15

Cys Arg Phe Gln Gly Thr Asn Phe Ser Pro Leu Tyr Val Tyr Ser Xaa
20 25 30

<210> 103
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (28)
<223> Xaa equals stop translation

<400> 103
Met Ile Ile Ala Pro Ile Cys Leu Ile Pro Phe Leu Ile Thr Leu Val
1 5 10 15

Val Trp Arg Ser Lys Asp Ser Glu Ala Gln Ala Xaa
20 25

<210> 104
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (87)
<223> Xaa equals stop translation

<400> 104
Met Gly Val Leu Ala Glu His Gly Gly His Pro Ala Gln Glu His Phe
1 5 10 15

Pro Lys Leu Leu Gly Leu Leu Phe Pro Leu Leu Ala Arg Glu Arg His
20 25 30

Asp Arg Val Arg Asp Asn Ile Cys Gly Ala Leu Ala Arg Leu Leu Met
35 40 45

Ala Ser Pro Thr Arg Lys Xaa Arg Ala Pro Gly Ala Gly Cys Pro Thr
50 55 60

Ala Cys Pro Ala Thr Glu Gly Gly Leu Gly Gly Val Gly Gln Pro Leu
65 70 75 80

Gly Ala Ser Ser Ala Ser Xaa
85

<210> 105
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (128)
<223> Xaa equals stop translation

<400> 105
Met Lys Val Ala Phe Leu Leu Gly Ser Leu Ala Ala Arg Gly Ser Asp
1 5 10 15

Thr Arg Ser Asn Thr Glu Leu Ser Ser Gly Ala Lys Val Phe Pro Val
20 25 30

Ser Ser Ala Arg Glu Pro Ser Pro Pro Ala Ser Phe Arg Ser Gln Cys
35 40 45

Ser Ser Asn Thr Val Tyr Thr Leu Phe Cys Phe Gln Ile Tyr Pro Glu
50 55 60

Ala Leu Leu Ser Ile Asn Asp Tyr Thr Ile Lys Val Ser Val Ile Leu
65 70 75 80

Glu Leu Ile Ser Val Gly Ile [illegible] In Ser Val Ala Phe Arg
85 95

Gly Leu Ser Pro Ile Leu Val [illegible] Ser Leu His

100 105 110

Leu Asp Leu Asn Glu Gly Leu Trp Leu Glu Cys Val Arg Ser Arg Xaa
115 120 125

<210> 106
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (31)
<223> Xaa equals stop translation

<400> 106
Met Arg Lys Glu Glu Gln Val Phe Phe Val Met Leu Leu Arg Lys Tyr
1 5 10 15

Pro Glu Ser Gln His His Asp Leu Leu Val Lys Gln Asn Lys Xaa
20 25 30

<210> 107
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (32)
<223> Xaa equals stop translation

<400> 107
Met Arg Ile Val Val Leu Val Thr Phe Met Cys Leu Gly Arg Leu Arg
1 5 10 15

Cys Ser Thr Ser Leu Arg His Ser Gln Asn Ala Asn Leu Leu Phe Xaa
20 25 30

<210> 108
<211> 96
<212> PRT
<213> Homo sapiens

<400> 108
[illegible] Ser Asn Gln Ser Ser Thr Cys Met Lys Thr Leu
1 5 10 15

Ser Trp Arg Ala Gln Gly His Ala Ala Gly Phe

55

20 25 30

Leu Lys Ile Lys Ala Leu Phe Leu Lys Tyr Met Ala Thr Lys Asp Ala
35 40 45

Phe Leu Gly Ser Asp Val Ser Trp Leu Ile Gln Ile Ile Met Met Val
50 55 60

Leu Gly Asn Phe Tyr Asn Tyr Arg Pro Leu Leu Phe Phe Met Leu Asn
65 70 75 80

Ala Ser Cys Arg Ile Arg Tyr Gln Ala Tyr Arg Tyr Arg Arg Pro Arg
85 90 95

<210> 109
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals stop translation

<400> 109
Met Tyr Phe Ile Tyr Leu Lys Tyr Ile Leu Leu Thr Pro Gly Val Gly
1 5 10 15

Met Asn Glu Thr Arg Xaa
20

<210> 110
<211> 46
<212> PRT
<213> Homo sapiens

<400> 110
Met Leu Val Leu Glu Asn Lys Phe Lys Ser Phe Leu Tyr Val Ile Tyr
1 5 10 15

Thr Leu Pro Glu Lys Ser Leu Asn Ser Ile Glu Asn Asp Leu Phe Phe
20 25 30

Glu Asp Leu Thr Asn Phe Thr Cys Lys Ser Val Cys Ala Leu
35 40 45

<210> 111
<211> 356
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (356)
<223> Xaa equals stop translation

<400> 111

```
Met Phe Tyr Leu Leu Leu Ser Leu Leu Met Ile Lys Val Lys Ser Ser
 1               5                  10                  15

Ser Asp Pro Arg Ala Ala Val His Asn Gly Phe Trp Phe Phe Lys Phe
            20                  25                  30

Ala Ala Ala Ile Ala Ile Ile Ile Gly Ala Phe Phe Ile Pro Glu Gly
        35                  40                  45

Thr Phe Thr Thr Val Trp Phe Tyr Val Gly Met Ala Gly Ala Phe Cys
    50                  55                  60

Phe Ile Leu Ile Gln Leu Val Leu Leu Ile Asp Phe Ala His Ser Trp
65                  70                  75                  80

Asn Glu Ser Trp Val Glu Lys Met Glu Glu Gly Asn Ser Arg Cys Trp
                85                  90                  95

Tyr Ala Ala Leu Leu Ser Ala Thr Ala Leu Asn Tyr Leu Leu Ser Leu
            100                 105                 110

Val Ala Ile Val Leu Phe Phe Val Tyr Tyr Thr His Pro Ala Ser Cys
        115                 120                 125

Ser Glu Asn Lys Ala Phe Ile Ser Val Asn Met Leu Leu Cys Val Gly
    130                 135                 140

Ala Ser Val Met Ser Ile Leu Pro Lys Ile Gln Glu Ser Gln Pro Arg
145                 150                 155                 160

Ser Gly Leu Leu Gln Ser Ser Val Ile Thr Val Tyr Thr Met Tyr Leu
                165                 170                 175

Thr Trp Ser Ala Met Thr Asn Glu Pro Glu Thr Asn Cys Asn Pro Ser
            180                 185                 190

Leu Leu Ser Ile Ile Gly Tyr Asn Thr Thr Ser Thr Val Pro Lys Glu
        195                 200                 205

Gly Gln Ser Val Gln Trp Trp His Ala Gln Gly Ile Ile Gly Leu Ile
    210                 215                 220

Leu Phe Leu Leu Cys Val Phe Tyr Ser Ser Ile Arg Thr Ser Asn Asn
225                 230                 235                 240

Ser Gln Val Asn Lys Leu Thr Leu Thr Ser Asp Glu Ser Thr Leu Ile
                245                 250                 255

Glu Asp Gly Gly Ala Arg Ser Asp Gly Ser Leu Gly Asp Asp
            260                 265

Val His Arg Ala Val Asp Asn Glu Arg Asn                 Ser Tyr
        275                 280
```

```
Ser Phe Phe His Phe Met Leu Phe Leu Ala Ser Leu Tyr Ile Met Met
    290                 295                 300

Thr Leu Thr Asn Trp Tyr Arg Tyr Glu Pro Ser Arg Glu Met Lys Ser
305                 310                 315                 320

Gln Trp Thr Ala Val Trp Val Lys Ile Ser Ser Ser Trp Ile Gly Ile
                325                 330                 335

Val Leu Tyr Val Trp Thr Leu Val Ala Pro Leu Val Leu Thr Asn Arg
            340                 345                 350

Asp Phe Asp Xaa
        355
```

<210> 112
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (71)
<223> Xaa equals stop translation

<400> 112

```
Met His Trp Leu Gly Arg Gly Trp Arg Leu Leu Glu Gly Gly Glu Lys
  1               5                  10                  15

Glu Leu Pro Thr Trp Ser Leu Leu Leu Leu Tyr Pro Gly Cys Leu Gln
            20                  25                  30

Ser Cys Ser Thr Thr Pro Trp Thr Thr Pro Ser Gln Met Pro Glu Ala
        35                  40                  45

Thr Gly Gly Gln Gly Arg Gln Gly Gly Leu Pro Ala Leu Leu Gln Gln
    50                  55                  60

Arg Ala Thr Thr Leu Gly Xaa
65                  70
```

<210> 113
<211> 171
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (171)
<223> Xaa equals stop translation

<400> 113

```
Met Val Pro V                 er Leu Leu Leu Leu Gly Pro Ala Val
  1                                 10                  15
```

Pro Gln Glu Asn Gln Asp Gly Arg Tyr Ser Leu Thr Tyr Ile Tyr Thr
20 25 30

Gly Leu Ser Lys His Val Glu Asp Val Pro Ala Phe Gln Ala Leu Gly
35 40 45

Ser Leu Asn Asp Leu Gln Phe Phe Arg Tyr Asn Ser Lys Asp Arg Lys
50 55 60

Ser Gln Pro Met Gly Leu Trp Arg Gln Val Glu Gly Met Glu Asp Trp
65 70 75 80

Lys Gln Asp Ser Gln Leu Gln Lys Ala Arg Glu Asp Ile Phe Met Glu
85 90 95

Thr Leu Lys Asp Ile Val Glu Tyr Tyr Asn Asp Ser Asn Gly Ser His
100 105 110

Val Leu Gln Gly Arg Phe Gly Cys Glu Ile Glu Asn Asn Arg Ser Ser
115 120 125

Gly Ala Phe Trp Lys Tyr Tyr Tyr Asp Gly Lys Asp Tyr Ile Glu Phe
130 135 140

Asn Lys Glu Ile Pro Ala Trp Val Pro Phe Asp Pro Ala Ala Gln Ile
145 150 155 160

Thr Lys Gln Lys Trp Asp Ala Cys Leu Glu Xaa
165 170

<210> 114
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (36)
<223> Xaa equals stop translation

<400> 114
Met Gly Leu Phe Asn Gln Cys Asp Tyr Ser Asp Pro Ser Leu Gln Leu
1 5 10 15

Val Phe Phe Leu Met Ala Leu Phe His Ile Leu Phe Ser Leu Thr Thr
20 25 30

Leu Ile Met Xaa
35

<210> 115
<211> 14
<212> PRT
<213> Homo sapiens

<221> SITE
<222> (14)
<223> Xaa equals stop translation

<400> 115
Met Arg Asp His Glu Ile Trp Glu Gly Pro Gly Ala Glu Xaa
1 5 10

<210> 116
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (156)
<223> Xaa equals stop translation

<400> 116
Met Phe Glu His Phe Ser Leu Phe Phe Val Cys Val Phe Gln Ile Asn
1 5 10 15

Val Phe Phe Tyr Thr Ile Pro Leu Ala Ile Lys Leu Lys Glu His Pro
20 25 30

Ile Phe Phe Met Phe Ile Gln Ile Ala Val Ile Ala Ile Phe Lys Ser
35 40 45

Tyr Pro Thr Val Gly Asp Val Ala Leu Tyr Met Ala Phe Phe Pro Val
50 55 60

Trp Asn His Leu Tyr Arg Phe Leu Arg Asn Ile Phe Val Leu Thr Cys
65 70 75 80

Ile Ile Ile Val Cys Ser Leu Leu Phe Pro Val Leu Trp His Leu Trp
85 90 95

Ile Tyr Ala Gly Ser Ala Asn Ser Asn Phe Phe Tyr Ala Ile Thr Leu
100 105 110

Thr Phe Asn Val Gly Gln Ile Leu Leu Ile Ser Asp Tyr Phe Tyr Ala
115 120 125

Phe Leu Arg Arg Glu Tyr Tyr Leu Thr His Gly Leu Tyr Leu Thr Ala
130 135 140

Lys Asp Gly Thr Glu Ala Met Leu Val Leu Lys Xaa
145 150 155

<210> 117
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (39)
<223> Xaa equals stop translation

<400> 117
Met Val Cys Glu Leu Ala His Leu Asp His Cys Ile Leu Pro Leu Ser
1 5 10 15

Phe Leu Val Ser His Cys His Cys Met Ala Ser Cys His Cys Glu Ser
20 25 30

Trp Pro Ser Leu Ser Leu Xaa
35

<210> 118
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (46)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (47)
<223> Xaa equals stop translation

<400> 118
Met Glu Val Val Leu Thr Val Ala His Pro Leu Arg Glu Arg Arg Lys
1 5 10 15

Arg Ser Ser Val Ile Cys Val Tyr Cys Cys Leu Leu Phe Cys Leu Phe
20 25 30

Tyr Tyr Val Val Phe Ile Asp Phe Val Lys Lys Val Asn Xaa Xaa
35 40 45

<210> 119
<211> 147
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (70)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (147)
<223> Xaa equals stop translation

<400> 119
Met Lys Ala Ser Val Val Leu [illegible] Glu Gly Tyr Leu Val Val Pro
1 5 15

```
Ser Gly Ala Tyr Ile Leu Gly Arg Cys Thr Val Ala Lys Lys Leu His
            20                  25                  30

Asp Gly Gly Leu Asp Tyr Phe Glu Gly Tyr Ser Leu Glu Asn Trp Val
        35                  40                  45

Cys Leu Ala Tyr Phe Glu Ser Lys Phe Asn Pro Met Ala Ile Tyr Glu
    50                  55                  60

Asn Thr Arg Glu Gly Xaa Thr Gly Phe Gly Leu Phe Gln Met Arg Gly
65                  70                  75                  80

Ser Asp Trp Cys Gly Asp His Gly Arg Asn Arg Cys His Met Ser Cys
                85                  90                  95

Ser Ala Leu Leu Asn Pro Asn Leu Glu Lys Thr Ile Lys Cys Ala Lys
            100                 105                 110

Thr Ile Val Lys Gly Lys Glu Gly Met Gly Ala Trp Pro Thr Trp Ser
        115                 120                 125

Arg Tyr Cys Gln Tyr Ser Asp Thr Leu Ala Arg Trp Leu Asp Gly Cys
    130                 135                 140

Lys Leu Xaa
145
```

<210> 120
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (44)
<223> Xaa equals stop translation

<400> 120

```
Met Tyr Leu Ser His Phe His Leu Gly Ile Val Ile Met Ala Val Ala
  1               5                  10                  15

Ala Leu Met Glu Lys Pro Val Leu Ala Ser Phe Ser Gly Ile Arg Ile
            20                  25                  30

Ser Cys His Arg Thr Ile Gly Lys Val Gln Val Xaa
        35                  40
```

<210> 121
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (81)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (52)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (81)
<223> Xaa equals stop translation

<400> 121
Met Ser Lys Gly Arg Pro Lys Leu Gly Ser Ser Lys Gly Leu Ala Gly
1 5 10 15

Gln Leu Trp Leu Leu Thr Leu Arg Leu Leu Leu Gly Ala Leu Leu Val
20 25 30

Trp Thr Xaa Ala Tyr Val Tyr Val Val Asn Pro Thr Pro Phe Glu Gly
35 40 45

Leu Val Pro Xaa Leu Leu Ser Arg Ala Thr Val Trp Lys Leu Arg Ala
50 55 60

Leu Leu Asp Pro Phe Leu Arg Leu Lys Xaa Asp Gly Phe Leu Pro Phe
65 70 75 80

Xaa

<210> 122
<211> 98
<212> PRT
<213> Homo sapiens

<400> 122
Met Cys Ser Val Val Leu Leu Lys Asp Cys Pro Leu Phe Ser Phe Ser
1 5 10 15

Val Ile Asn Gly His Thr Leu Cys Leu Arg Leu Leu Leu Glu Ile Ala
20 25 30

Asp Asn Pro Glu Ala Val Asp Val Lys Asp Ala Lys Gly Gln Thr Pro
35 40 45

Leu Met Leu Ala Val Ala Tyr Gly His Ile Asp Ala Val Ser Leu Leu
50 55 60

Leu Glu Lys Glu Ala Asn Val Asp Thr Val Asp Ile Leu Gly Cys Th
65 70 75 8

Ala Leu His Arg Gly Val Cys Thr Ser Phe Ser Ala Leu Val Lys Gln
85 90 95

Phe Phe

<210> 123
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (32)
<223> Xaa equals stop translation

<400> 123
Met Asn Cys Val Leu Ala Thr Tyr Gly Ser Ile Ala Leu Ile Val Leu
1 5 10 15

Tyr Phe Lys Leu Arg Ser Lys Lys Thr Pro Ala Val Lys Ala Thr Xaa
20 25 30

<210> 124
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals stop translation

<400> 124
Met Asn Gly Leu Leu Phe Leu Val Met Ile Ala Lys Asn Leu Leu Pro
1 5 10 15

Ser Gly Asn Lys Gln Xaa
20

<210> 125
<211> 121
<212> PRT
<213> Homo sapiens

<400> 125
Met Leu Trp Val Lys Thr Arg Arg Glu Glu Leu Arg Pro Phe Gly Glu
1 5 10 15

Pro Arg Pro Gly Ser Ser Leu Arg [illegible] Leu Phe Gly
20 30

Pro Leu Lys Phe Leu Glu Ser Gln Ala Ser Ser Arg His His Val Ser
35 40 45

Trp Trp Gln Leu Trp Lys Leu Leu Leu Val Cys Leu Val Gln Leu Gln
50 55 60

Pro Cys Arg Glu Pro Ala Pro Met Gln Thr Pro Cys Ala Gly Cys Pro
65 70 75 80

Ala Ala Ala Ala Gly Val Pro His Cys Val Gln Trp Leu Asp Pro Met
85 90 95

Leu Thr Cys Ser His Thr Pro His Cys Ser Thr Pro Gly Leu Pro Leu
100 105 110

Ala Val Met Gly Ser Arg Leu Val Ala
115 120

<210> 126
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (26)
<223> Xaa equals stop translation

<400> 126
Met Leu Pro Ser Phe Pro Ser Leu Arg Val Phe Val Ile Phe Phe Cys
1 5 10 15

Leu Leu Val Tyr Cys Leu Phe Ala Pro Xaa
20 25

<210> 127
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (24)
<223> Xaa equals stop translation

<400> 127
Met Pro Se Thr Val Ser Leu Gly Arg Gly His Phe Xaa Phe
1 10 15

Cys Ser Pl o Ile Xaa

<210> 128
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (39)
<223> Xaa equals stop translation

<400> 128
Met Tyr Lys Ile His Ser Glu Asn Cys Leu Val Ile Leu His Leu Phe
1 5 10 15

Ile Gln Lys Thr Val Ile Ser Gly Glu Pro Asn Met Leu Val Asn Ile
20 25 30

Phe Asn Phe Phe Pro His Xaa
35

<210> 129
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (74)
<223> Xaa equals stop translation

<400> 129
Met Gly Ile Ala Val Ser Met Leu Thr Tyr Pro Phe Leu Leu Val Gly
1 5 10 15

Asp Leu Met Ala Val Asn Asn Cys Gly Leu Gln Ala Gly Leu Pro Pro
20 25 30

Tyr Ser Pro Val Phe Lys Ser Trp Ile His Cys Trp Lys Tyr Leu Ser
35 40 45

Val Gln Gly Gln Leu Phe Arg Gly Ser Ser Leu Leu Phe Arg Arg Val
50 55 60

Ser Ser Gly Ser Cys Phe Ala Leu Glu Xaa
65 70

<210> 130
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (55)

<223> Xaa equals stop translation

<400> 130
Met His Ser Gly Phe Tyr Thr Ser Ala Phe Arg Gly Leu Trp Gln His
1 5 10 15

Gly Met Gly Gln Glu Val Leu Leu Leu His Leu Pro Leu Met Ser Val
20 25 30

Thr His Pro Phe Cys Thr Ala Gly Val Val Asn Ala Phe Val Ser Ser
35 40 45

Ser Ser His Ala Asp Cys Xaa
50 55

<210> 131
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (44)
<223> Xaa equals stop translation

<400> 131
Met Glu Leu Arg Val Glu Thr Gly His Phe Thr Gly His Leu Ser Thr
1 5 10 15

Val Lys Ile Leu Phe Thr Leu Leu Val Pro Val Phe Tyr Ile Glu Asp
20 25 30

Leu Ala Met Asn Cys Tyr Leu Asn Leu Arg Ala Xaa
35 40

<210> 132
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (37)
<223> Xaa equals stop translation

<400> 132
Met Phe Phe Gly Ala Pro Thr Ala Gly Ala Val Gln Val Trp Leu Leu
1 5 10 15

Leu Leu Ser Pro Ala Ala Ser Pro Val Glu Glu Leu Ser Val Leu Val
20 25 30

Pro Cys Gly Gln Xaa
35

<210> 133
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (50)
<223> Xaa equals stop translation

<400> 133
Met Ile Leu Leu Pro Gly Leu Ser His Tyr Asn Ala Leu Gly Leu Phe
1 5 10 15

Phe Ala Ala Val Leu Leu Phe Leu Asn Leu Gly Gln Val Pro Met Leu
20 25 30

Ala Val Arg Arg Asp Ser Val His Ser Thr Cys Asn Phe Arg Glu Trp
35 40 45

Lys Xaa
50

<210> 134
<211> 84
<212> PRT
<213> Homo sapiens

<400> 134
Met Asn Pro Leu Cys Pro Pro Leu Leu Leu Leu Asp Leu Gln Thr Gln
1 5 10 15

Cys Pro Gln Arg Cys Ser Tyr Ile Leu Tyr Ser Cys Phe Ser Gly Met
20 25 30

Val Leu Met Pro Pro Lys Ala Pro Ala Cys Glu Ser Thr Phe Val Phe
35 40 45

Ile Ser Trp Ser Pro Leu Ser Ser Leu Val Pro Pro Arg Pro Ser Phe
50 55 60

His His Leu Pro Arg His Ser Glu Leu Asp Gln Tyr Leu Cys Gly Arg
65 70 75 80

Leu Gly Val Thr

<210> 135
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> S
<222> (
<223> : nslation

<400> 135
Met Leu Leu Val Asn Leu Val Phe Val Cys Phe Phe Leu Phe Glu Arg
1 5 10 15

Arg Val His Leu Lys Cys Xaa
20

<210> 136
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (45)
<223> Xaa equals stop translation

<400> 136
Met Met Gly Ile Leu Phe Ile His Leu Phe Ile Tyr Leu Phe Thr Glu
1 5 10 15

Asp Trp Phe Leu Pro Val Gln Phe Asn Ser Phe Ser Glu Val Ser Ile
20 25 30

Met Ile Arg Lys Ile Asp Cys Ser Tyr Tyr Ser Lys Xaa
35 40 45

<210> 137
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (47)
<223> Xaa equals stop translation

<400> 137
Met Met Leu Leu Leu Ala Ser Ala Phe Leu Ile Gly Thr Val Leu Gly
1 5 10 15

Ser Asn Arg Ser Cys Met Ser Gln Cys Cys Gly His His Lys Ser Gln
20 25 30

Lys Ala Gln Lys Thr Ser Ser Phe Ile Thr Ala Pro Val Lys Xaa
35 40 45

<210> 138
<211> 288
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (23)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 138

```
Met Lys Thr Leu Ala Thr Gly Thr Lys Asn Arg Arg Arg Arg Pro Ala
 1               5                  10                  15

Ala Ala Ala Ala Ala Cys Xaa Val Gln Gly Pro Glu Pro Ala Arg Val
            20                  25                  30

Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp
        35                  40                  45

Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala
    50                  55                  60

Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile
65                  70                  75                  80

Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly
                85                  90                  95

Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly
            100                 105                 110

Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr
        115                 120                 125

Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys
    130                 135                 140

Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu
145                 150                 155                 160

Leu Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly
                165                 170                 175

Pro Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys
            180                 185                 190

Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr
        195                 200                 205

Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu
    210                 215                 220

Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly
225                 230                 235                 240

His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala
                245                 250                 255

Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly [illegible] Phe
            260                 265

Leu Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro As[illegible] Phe
        275                 280                 28[illegible]
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<210> 139
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (24)
<223> Xaa equals stop translation

<400> 139
Met Phe Leu Phe Leu Phe Phe Leu Leu Ile Ile Ala Ser Tyr Ile Ser
1 5 10 15

Ser Phe Ser Phe Gly Gln Ser Xaa
20

<210> 140
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (54)
<223> Xaa equals stop translation

<400> 140
Met Val Leu Leu Leu Leu Gln Arg Asn Pro Gly Thr Pro Leu Phe
1 5 10 15

Cys Leu Val Phe Trp Ala Gly Leu Arg Lys Pro Ala Gln Phe Arg Pro
20 25 30

Ile Leu Gly Pro Ser Cys Pro Cys Ala Ala Ser Val Lys Arg Gly Val
35 40 45

Asp Ile Pro Ser Ser Xaa
50

<210> 141
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (51)
<223> Xaa equals any [illegible] ly occurring L-amino acids

<220>
<221> SITE

<222> (61)
<223> Xaa equals stop translation

<400> 141
Met Leu Leu Glu Ser Trp Met Gly Ile Trp Gly Glu Arg Gly Arg Thr
1 5 10 15

Gly Gln Val Ser Pro Ser Pro Phe Cys Ser Cys Leu Leu Val Ser Ala
20 25 30

Leu Leu Glu Leu His Leu Pro Leu Gly Phe Ser Ala Pro Ala His Phe
35 40 45

Pro Ser Xaa Phe Thr Cys Phe Val Ser Phe Pro Cys Xaa
50 55 60

<210> 142
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (101)
<223> Xaa equals stop translation

<400> 142
Met Gly Asp Asp Gly Ser Ile Asp Tyr Thr Val His Glu Ala Trp Asn
1 5 10 15

Glu Ala Thr Asn Val Tyr Leu Ile Val Ile Leu Val Ser Phe Gly Leu
20 25 30

Phe Met Tyr Ala Lys Arg Asn Lys Arg Arg Ile Met Arg Ile Phe Ser
35 40 45

Val Pro Pro Thr Glu Glu Thr Leu Ser Glu Pro Asn Phe Tyr Asp Thr
50 55 60

Ile Ser Lys Ile Arg Leu Arg Gln Gln Leu Glu Met Tyr Ser Ile Ser
65 70 75 80

Arg Lys Tyr Asp Tyr Gln Gln Pro Gln Asn Gln Ala Asp Ser Val Gln
85 90 95

Leu Ser Leu Glu Xaa
100

<210> 143
<211> 42
<212> PRT
<213> Homo sapiens

<223> Xaa equals stop translation

<400> 143
Met Phe Ala Phe Leu Leu Gly Ile Tyr Leu Gly Val Lys Leu Leu Asp
1 5 10 15

Asn Met Phe Asn Tyr Leu Arg Thr Asp Arg Leu Leu Cys Lys Val Ala
20 25 30

Asn Met Ser Lys Phe Ser Ser His Leu Xaa
35 40

<210> 144
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (63)
<223> Xaa equals stop translation

<400> 144
Met Phe Gly Cys Arg Ala Val Lys Thr Gln Lys Glu Thr Leu Pro Ser
1 5 10 15

Ala Pro Gly Ser Pro Pro Leu Val Ala Leu Phe Ser Val Ala Leu Trp
20 25 30

Pro Val Ala Leu Ser Asn Glu Ala Thr Pro His Ser Cys Gly Gln Ala
35 40 45

Pro Gly Ala Pro Gly Gln Met Arg Thr Leu Phe Pro Pro Thr Xaa
50 55 60

<210> 145
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (33)
<223> Xaa equals stop translation

<400> 145
Met Val Phe His Leu Pro Leu Ser Asp Leu Phe Phe Met Leu Leu Leu
1 5 10 15

Ala Pro Lys Lys Ser Arg Met Ala Lys Glu Pro Arg Thr Tyr Trp Asn
20 25 30

Xaa

<210> 146
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (42)
<223> Xaa equals stop translation

<400> 146
Met Lys Val Gln Leu Ser Leu Gly Asn Pro Arg Gly Gln Gln Arg Thr
1 5 10 15

Pro Glu Leu Ile Gln Ala Leu Leu Leu Val Leu Asn Tyr Thr Leu Gly
20 25 30

Phe Phe Leu Leu Ser Lys Thr Phe His Xaa
35 40

<210> 147
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (41)
<223> Xaa equals stop translation

<400> 147
Met Asn Glu Ala Thr Met Ala Phe Ser Val Leu Ile Leu Pro Val Phe
1 5 10 15

Tyr Ala Gln Ile Arg Asn Lys Ser Phe Leu Cys Leu Ser Asp Ile Leu
20 25 30

Pro Leu Xaa Leu Ile Leu Leu Phe Xaa
35 40

<210> 148
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (44)
<223> Xaa equals stop translation

<400> 148

74

Met Asn Trp Tyr His Glu Asn Lys Glu Ala Thr Cys Asn Cys Gln Ile
1 5 10 15

Phe Gly Leu Tyr Phe Ile Val Ser Phe Leu Ser Pro Val Leu Ala Ala
20 25 30

Ala His Asp Ala Lys Lys Tyr Pro Val Trp Leu Xaa
35 40

<210> 149
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (55)
<223> Xaa equals stop translation

<400> 149
Met Pro Gly Pro Gly Ala Leu Tyr Ser Ser Phe Thr Ser Phe Tyr Tyr
1 5 10 15

Thr Phe Ser Asn His Gln Leu Leu Leu Ala Leu Leu Leu Leu Gly Phe
20 25 30

Ile Ala Ser Cys Ser Phe Phe Leu Ser Arg Val Phe Leu Thr Phe Ser
35 40 45

Thr Gln Leu Trp Lys Lys Xaa
50 55

<210> 150
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (100)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 150
Met Ser Lys Ser Glu Gln Cys Arg Ala Ala Cys Pro Ala Ala Leu Glu
1 5 10 15

Gln Glu Leu Ser Leu Gly Arg Gly Trp Trp Gly Trp Ala Thr Glu Gly
20 25 30

Ile Gly Ser Gln Ile His Pro Val Ser Pro Pro Ala Ser Pro Lys Gln
35 40 45

Ser [illegible] Glu Gln Ser Met Trp Asp Arg Cys Asn Ser Tyr Thr
55 60

H [illegible] Asp Arg Leu Arg Pro Pro Pro Val Leu Pro

75
65 70 75 80

Pro Ser Ile Tyr Thr Ile Arg Thr Cys Ser Gln Arg Leu Phe Ala Ala
85 90 95

Ala Gln Ser Xaa Ser Tyr Ser His Met Asn Val Arg Gly Pro Leu Ile
100 105 110

Gln Pro His Asn Thr Gln Gly Pro Phe Leu Thr Pro Ser Leu Ser Ser
115 120 125

Leu Leu Phe His Gln Ser Ser Pro Ala Cys Thr Leu Ser Ala Trp Pro
130 135 140

Leu Ser Arg Tyr Ala Gln Pro Gly Ser Ala Leu Leu Thr Thr Pro Pro
145 150 155 160

Arg Leu Gln Arg Gly
165

<210> 151
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (114)
<223> Xaa equals stop translation

<400> 151
Met Gly Trp Lys Leu Leu Gly Leu Leu Ser Ala Ala Gly Arg His Ser
1 5 10 15

Ala Gly Gly Asp Gln Ala Phe Pro Arg Pro Lys Gly Glu Ala Glu Ser
20 25 30

Ala Ser Pro Glu Pro Asp Ala Gly Leu Gly Phe Thr Leu His Gly Pro
35 40 45

Asp Val Lys Ser Asn Gly Asp Met Arg Phe Leu Met Ser Leu His Leu
50 55 60

Gln Met Tyr Thr Ser Ala Lys Leu His His Thr Asn Leu Thr Ala Gly
65 70 75 80

Pro Gly Phe Pro Leu Ser Arg Phe His Gln Pro Pro Pro Ser Val Leu
85 90 95

Ala Ala Cys Pro Ser Thr Asn Gln Leu Ser Pro Ala Pro Gly Asp Pro
100 105 110

Arg Xaa

<210> 152

<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (40)
<223> Xaa equals stop translation

<400> 152
Met Ala Leu Thr Trp Arg Val Val Leu Val Val Leu Phe Leu Ser Asp
1 5 10 15

Cys Gly Leu Lys His Lys Cys Pro Lys Val Gly Arg Leu Leu Ser Val
20 25 30

Ile Ile Val Ala Ile Lys Phe Xaa
35 40

<210> 153
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (64)
<223> Xaa equals stop translation

<400> 153
Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln Met Phe Phe Gly Ile
1 5 10 15

Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp Leu Val Phe
20 25 30

Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly Tyr Trp Leu
35 40 45

Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys Gly Arg Xaa
50 55 60

<210> 154
<211> 118
<212> PRT
<213> Homo sapiens

<400> 154
Met Val Ala Ile Pro Pro Ser Ala Cys Leu Pro Ala Cys Cys Pro Gly
1 5 10 15

His Gly Ala Val Pro Val Pro Arg Ile Gly Phe Lys Asn Asn
20 25

Phe Pro Phe Gly Leu Val Asp Val Asn Arg Ala Arg Glu Val Leu Pro
35 40 45

Thr Ala Cys Ala Cys Leu Pro Ala Ser Ser Leu Phe Ser Phe His Tyr
50 55 60

Ala Pro Ser Pro Gly Gly Leu Ala Leu Ser Phe Ser Ser Tyr Pro Gln
65 70 75 80

Gly Pro Val Leu Leu Cys Pro His Val Pro Leu Gly Cys Leu Val Glu
85 90 95

Ala Leu Tyr Asn Phe Ser Leu Val Leu Cys Ser Phe Leu Leu Tyr Phe
100 105 110

Pro Ala Val Ser Cys Pro
115

<210> 155
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (28)
<223> Xaa equals stop translation

<400> 155
Met His Ser Phe Thr Gln Arg Gly Met Tyr Ile Phe Leu Ser Ser Ser
1 5 10 15

Gln Ala Ile Phe Leu Met Ser Cys Phe Leu Phe Xaa
20 25

<210> 156
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (46)
<223> Xaa equals stop translation

<400> 156
Met Val Leu Ile Phe Leu Leu Val Gln Asn Arg Cys Ala Val Gly Ser
1 5 10 15

Thr Met Gln Phe Ser Phe Ser Thr Asp Pro Phe Leu Arg Asn Thr Asn
20 25 30

Phe Leu Leu [illegible] Val Leu Arg Cys Leu Pro Xaa
35 40 45

<210> 157
<211> 51
<212> PRT
<213> Homo sapiens

<400> 157
Phe Ile Thr Pro Glu Asp Gly Ser Lys Asp Val Phe Val His Phe Ser
1 5 10 15

Ala Ile Ser Ser Gln Gly Phe Lys Thr Leu Ala Glu Gly Gln Arg Val
20 25 30

Glu Phe Glu Ile Thr Asn Gly Ala Lys Gly Pro Ser Ala Ala Asn Val
35 40 45

Ile Ala Ile
50

<210> 158
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (37)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (54)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 158
Arg Ala Gly Gly Pro Arg Leu Pro Arg Thr Arg Val Gly Arg Pro Ala
1 5 10 15

Ala Leu Arg Leu Leu Leu Leu Leu Gly Ala Val Leu Asn Pro His Glu
20 25 30

Ala Leu Ala Gln Xaa Leu Pro Thr Thr Gly Thr Pro Gly Ser Glu Gly
35 40 45

Gly Thr Val Lys Asn Xaa Glu Thr Ala Val Gln Phe Cys Trp Asn His
50 55 60

Tyr Lys Asp Gln Met Asp Pro Ile Glu Lys Asp Trp Cys Asp Trp Ala
65 70 75 80

Met Ile Ser Arg Pro Tyr Ser Thr Leu Arg Asp Cys Leu Glu His Phe
85 90 95

Ala Glu Leu Phe Asp Leu Gly Phe Pro Asn Pro Leu Ala Glu Arg Ile
100 105 110

Ile Phe Glu Thr His Gln Ile His Phe Ala Asn Cys Ser Leu Val Gln

115 120 125

Pro Thr Phe Ser Asp Pro Pro Glu Asp Val Leu Leu Ala
130 135 140

<210> 159
<211> 60
<212> PRT
<213> Homo sapiens

<400> 159
Cys Trp Asn His Tyr Lys Asp Gln Met Asp Pro Ile Glu Lys Asp Trp
1 5 10 15

Cys Asp Trp Ala Met Ile Ser Arg Pro Tyr Ser Thr Leu Arg Asp Cys
20 25 30

Leu Glu His Phe Ala Glu Leu Phe Asp Leu Gly Phe Pro Asn Pro Leu
35 40 45

Ala Glu Arg Ile Ile Phe Glu Thr His Gln Ile His
50 55 60

<210> 160
<211> 48
<212> PRT
<213> Homo sapiens

<400> 160
Phe Ala Asn Cys Ser Leu Val Gln Pro Thr Phe Ser Asp Pro Pro Glu
1 5 10 15

Asp Val Leu Leu Ala Met Ile Ile Ala Pro Ile Cys Leu Ile Pro Phe
20 25 30

Leu Ile Thr Leu Val Val Trp Arg Ser Lys Asp Ser Glu Ala Gln Ala
35 40 45

<210> 161
<211> 10
<212> PRT
<213> Homo sapiens

<400> 161
Arg Ala Gly Gly Pro Arg Leu Pro Arg Thr
1 5 10

<210> 162
<211> 8
<212> PRT
<213> Homo sapiens

<400> 162
Asn Pro His Glu Ala Leu Ala Gln
1 5

<210> 163
<211> 118
<212> PRT
<213> Homo sapiens

<400> 163
Ala Gln Glu Arg Ser Cys Leu His Leu Val Cys Ile Arg Cys Ser Cys
1 5 10 15

Asp Val Val Glu Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser
20 25 30

Trp Ile Pro Cys Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys
35 40 45

Cys Pro Ser Gly Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu
50 55 60

Phe Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly
65 70 75 80

Met Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys
85 90 95

Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg
100 105 110

Leu Cys Phe Gly Leu Ala
115

<210> 164
<211> 74
<212> PRT
<213> Homo sapiens

<400> 164
Ile Pro Cys Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys
1 5 10 15

Pro Ser Gly Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe
20 25 30

Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly Met
35 40 45

Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys Gly
50 55 60

Val Val Pro Cys Asn Ile Leu Val Gly Tyr
65 70

<210> 165
<211> 95
<212> PRT
<213> Homo sapiens

<400> 165
Ala Arg Ser Asp Gly Ser Leu Glu Asp Gly Asp Asp Val His Arg Ala
1 5 10 15

Val Asp Asn Glu Arg Asp Gly Val Thr Tyr Ser Tyr Ser Phe Phe His
20 25 30

Phe Met Leu Phe Leu Ala Ser Leu Tyr Ile Met Met Thr Leu Thr Asn
35 40 45

Trp Tyr Arg Tyr Glu Pro Ser Arg Glu Met Lys Ser Gln Trp Thr Ala
50 55 60

Val Trp Val Lys Ile Ser Ser Ser Trp Ile Gly Ile Val Leu Tyr Val
65 70 75 80

Trp Thr Leu Val Ala Pro Leu Val Leu Thr Asn Arg Asp Phe Asp
85 90 95

<210> 166
<211> 28
<212> PRT
<213> Homo sapiens

<400> 166
Asn Glu Lys Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala
1 5 10 15

Val Tyr Arg Leu Cys Phe Gly Leu Ala Met Phe Tyr
20 25

<210> 167
<211> 19
<212> PRT
<213> Homo sapiens

<400> 167
Met Ile Lys Val Lys Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn
1 5 10 15

Gly Phe Trp

<210> 168
<211> 3
<212> PRT
<213> Homo sapiens

Gly Met Ala Gly Ala Phe Cys Phe Ile Leu Ile Gln Leu Val Leu Leu
1 5 10 15

Ile Asp Phe Ala His
20

<210> 169
<211> 24
<212> PRT
<213> Homo sapiens

<400> 169
Tyr Ala Ala Leu Leu Ser Ala Thr Ala Leu Asn Tyr Leu Leu Ser Leu
1 5 10 15

Val Ala Ile Val Leu Phe Phe Val
20

<210> 170
<211> 21
<212> PRT
<213> Homo sapiens

<400> 170
Pro Ser Leu Leu Ser Ile Ile Gly Tyr Asn Thr Thr Ser Thr Val Pro
1 5 10 15

Lys Glu Gly Gln Ser
20

<210> 171
<211> 22
<212> PRT
<213> Homo sapiens

<400> 171
Tyr Ser Ser Ile Arg Thr Ser Asn Asn Ser Gln Val Asn Lys Leu Thr
1 5 10 15

Leu Thr Ser Asp Glu Ser
20

<210> 172
<211> 20
<212> PRT
<213> Homo sapiens

<400> 172
Asp Asn Glu Arg Asp Gly Val Thr Tyr Ser Tyr Ser Phe Phe His Phe
1 5 10 15

Met Leu Phe Leu
20

<210> 173
<211> 18
<212> PRT
<213> Homo sapiens

<400> 173
Ile Val Leu Tyr Val Trp Thr Leu Val Ala Pro Leu Val Leu Thr Asn
1 5 10 15

Arg Asp

<210> 174
<211> 11
<212> PRT
<213> Homo sapiens

<400> 174
Asp Pro Arg Val Arg Ala Asp Thr Met Val Arg
1 5 10

<210> 175
<211> 45
<212> PRT
<213> Homo sapiens

<400> 175
Gly Pro Ala Val Pro Gln Glu Asn Gln Asp Gly Arg Tyr Ser Leu Thr
1 5 10 15

Tyr Ile Tyr Thr Gly Leu Ser Lys His Val Glu Asp Val Pro Ala Phe
20 25 30

Gln Ala Leu Gly Ser Leu Asn Asp Leu Gln Phe Phe Arg
35 40 45

<210> 176
<211> 21
<212> PRT
<213> Homo sapiens

<400> 176
Tyr Asn Ser Lys Asp Arg Lys Ser Gln Pro Met Gly Leu Trp Arg Gln
1 5 10 15

Val Glu Gly Met Glu
20

<210> 177
<211> 22
<212> PRT
<213> Homo sapiens

<400> 177
Phe Met Glu Thr Leu Lys Asp Ile Val Glu Tyr Tyr Asn Asp Ser Asn
1 5 10 15

Gly Ser His Val Leu Gln
20

<210> 178
<211> 20
<212> PRT
<213> Homo sapiens

<400> 178
Asn Arg Ser Ser Gly Ala Phe Trp Lys Tyr Tyr Tyr Asp Gly Lys Asp
1 5 10 15

Tyr Ile Glu Phe
20

<210> 179
<211> 71
<212> PRT
<213> Homo sapiens

<400> 179
Ile Arg His Glu Thr Glu Cys Gly Ile Asp His Ile Cys Ile His Arg
1 5 10 15

His Cys Val His Ile Thr Ile Leu Asn Ser Asn Cys Ser Pro Ala Phe
20 25 30

Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His His Cys His Cys Asn
35 40 45

Tyr Leu Trp Asp Pro Pro Asn Cys Leu Ile Lys Gly Tyr Gly Gly Ser
50 55 60

Val Asp Ser Gly Pro Pro Pro
65 70

<210> 180
<211> 11
<212> PRT
<213> Homo sapiens

<400> 180
Gly Ile Cys Asn Asn Lys His His Cys His Cys
1 5 10

<210> 181
<211> 145
<212> PRT
<213> Homo

<220>
<221> SITE
<222> (29)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (34)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 181
Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe Ile Leu Leu
1 5 10 15

Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Pro Xaa Lys Lys Gln
20 25 30

Gln Xaa Val Gln Thr Pro Ser Ala Lys Glu Glu Glu Lys Ile Gln Arg
35 40 45

Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val Met Pro Ser
50 55 60

Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser His Pro Gln Val Met
65 70 75 80

Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser Gln Pro Arg
85 90 95

Val Met Pro Ser Gln Ser Gln Pro Pro Val Met Pro Ser Gln Ser His
100 105 110

Pro Gln Leu Thr Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln
115 120 125

Arg Gln Pro Gln Leu Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro
130 135 140

Ser
145

<210> 182
<211> 234
<212> PRT
<213> Homo sapiens

<400> 182
Gly Ser Phe Arg Gly Thr Gly Arg Gly Arg Asp Gly Ala Gln His Pro
1 5 10 15

Leu Leu Tyr Val Lys Leu Leu Ile Gln Val Gly His Glu Pro Met Pro
20 25 30

Pro Thr Leu Gly Thr Asn Val Leu Gly Arg Lys Val Leu Tyr Leu Pro
35 40 45

Ser Phe Phe Thr Tyr Ala Lys Tyr Ile Val Gln Val Asp Gly Lys Ile

50 55 60

Gly Leu Phe Arg Gly Leu Ser Pro Arg Leu Met Ser Asn Ala Leu Ser
65 70 75 80

Thr Val Thr Arg Gly Ser Met Lys Lys Val Phe Pro Pro Asp Glu Ile
85 90 95

Glu Gln Val Ser Asn Lys Asp Asp Met Lys Thr Ser Leu Lys Lys Val
100 105 110

Val Lys Glu Thr Ser Tyr Glu Met Met Met Gln Cys Val Ser Arg Met
115 120 125

Leu Ala His Pro Leu His Val Ile Ser Met Arg Cys Met Val Gln Phe
130 135 140

Val Gly Arg Glu Ala Lys Tyr Ser Gly Val Leu Ser Ser Ile Gly Lys
145 150 155 160

Ile Phe Lys Glu Glu Gly Leu Leu Gly Phe Phe Val Gly Leu Ile Pro
165 170 175

His Leu Leu Gly Asp Val Val Phe Leu Trp Gly Cys Asn Leu Leu Ala
180 185 190

His Phe Ile Asn Ala Tyr Leu Val Asp Asp Ser Val Ser Asp Thr Pro
195 200 205

Gly Gly Leu Gly Asn Asp Gln Asn Pro Gly Ser Gln Phe Ser Gln Ala
210 215 220

Leu Ala Ile Arg Ser Tyr Thr Lys Phe Val
225 230

<210> 183
<211> 120
<212> PRT
<213> Homo sapiens

<400> 183
Ala Arg Ala Ala Pro Arg Leu Leu Leu Leu Phe Leu Val Pro Leu Leu
1 5 10 15

Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu Asp Leu Ser His
20 25 30

Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu Gln Pro Gln Pro
35 40 45

Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu Asp Pro Tyr Gly
50 55 60

Val Ala Val Gly Gly Thr Val Gly His Cys Leu
65 70 75

Val Ile Gly Gly Arg Met Ile Ala Gln Lys

87

85 90 95

Thr Ile Ile Gly Gly Ile Val Phe Leu Ala Phe Ala Phe Ser Ala Leu
100 105 110

Phe Ile Ser Pro Asp Ser Gly Phe
115 120

<210> 184
<211> 70
<212> PRT
<213> Homo sapiens

<400> 184
Phe Arg Ile Ala Trp Leu Leu Cys Leu Met Ile Cys Leu Ile Gln Lys
1 5 10 15

Gln Glu Cys Arg Val Lys Thr Glu Pro Met Asp Ala Asp Asp Ser Asn
20 25 30

Asn Cys Thr Gly Gln Asn Glu His Gln Arg Glu Asn Ser Gly His Arg
35 40 45

Arg Asp Gln Ile Ile Glu Lys Asp Ala Ala Leu Cys Val Leu Ile Asp
50 55 60

Glu Met Asn Glu Arg Pro
65 70

<210> 185
<211> 51
<212> PRT
<213> Homo sapiens

<400> 185
Arg Val Lys Thr Glu Pro Met Asp Ala Asp Asp Ser Asn Asn Cys Thr
1 5 10 15

Gly Gln Asn Glu His Gln Arg Glu Asn Ser Gly His Arg Arg Asp Gln
20 25 30

Ile Ile Glu Lys Asp Ala Ala Leu Cys Val Leu Ile Asp Glu Met Asn
35 40 45

Glu Arg Pro
50

<210> 186
<211> 26
<212> PRT
<213> Homo sapiens

<400> 186
Gln Val Ser Ala [illegible] Pro Met Gln Tyr Ile Lys Glu Tyr
1 10 15

Thr Asp Glu Asn Ile Gln Glu Gly Leu Ala
20 25

<210> 187
<211> 24
<212> PRT
<213> Homo sapiens

<400> 187
Ser Gln Gly Ile Glu Arg Leu His Pro Met Gln Phe Asp His Lys Lys
1 5 10 15

Glu Leu Arg Lys Leu Asn Met Ser
20

<210> 188
<211> 31
<212> PRT
<213> Homo sapiens

<400> 188
Leu Glu Thr Ala Glu Arg Phe Gln Lys His Leu Glu Arg Val Ile Glu
1 5 10 15

Met Ile Gln Asn Cys Leu Ala Ser Leu Pro Asp Asp Leu Pro His
20 25 30

<210> 189
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 189
Met Thr Met Ile Thr Pro Ser Ser Lys Leu Thr Leu Thr Lys Gly Asn
1 5 10 15

Lys Ser Trp Ser Ser Thr Ala Val Ala Ala Ala Leu Glu Leu Val Asp
20 25 30

Pro Pro Gly Cys Arg Asn Ser Pro Pro Pro Pro His Thr Pro Phe Ser
35 40 45

Tyr Ala Phe Gly Val Leu Asp Gly Asn Leu Gly Gly Glu Arg Lys Asp
50 55 60

Arg Ser Gly Leu Pro Gln Pro Leu Leu Leu Leu Ser Pro Arg Val Arg
65 70 75 80

Gly Ala Pro Pro Pro Ser Trp Phe Leu Arg Thr Arg Pro Phe

89
85 90 95

Ser Phe Cys Leu Tyr Leu Leu Arg Ile Leu Ser Leu Leu Met Trp Leu
100 105 110

Thr Pro Leu Pro Pro Leu Pro Ala Gly Gly Trp Pro Gly Gly Gln Val
115 120 125

Pro Ala Gly Ala Val Asn Arg Xaa Cys Ala Phe Val Leu Val Cys Ala
130 135 140

Cys Ala Val Phe Leu Cys Phe Asp Arg Ser
145 150

<210> 190
<211> 28
<212> PRT
<213> Homo sapiens

<400> 190
Leu Thr Leu Thr Lys Gly Asn Lys Ser Trp Ser Ser Thr Ala Val Ala
1 5 10 15

Ala Ala Leu Glu Leu Val Asp Pro Pro Gly Cys Arg
20 25